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OM protein - protein search, using sw model

Run on: October 8, 2004, 10:15:45 ; Search time 12 Seconds
(without alignments)
1466.643 Million cell updates/sec

Title: US-09-633-145-2
Perfect score: 1801
Sequence: 1 MFPCNNINISCVKNWNSND.....FGKIFQKSSRCKLFLLESS 338

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues
Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1801	100.0	339	1 TARI HUMAN	Q66rj0 homo sapien
2	1757	97.6	338	1 TARI MACMU	Q8hz64 macaca mula
3	1403	77.9	332	1 TARI RAT	Q923y9 rattus norv
4	1351	75.0	332	1 TARI MOUSE	Q923y8 mus musculu
5	927.5	51.5	347	1 TARI2 RAT	Q923y7 rattus norv
6	815	45.3	306	1 GP58 HUMAN	Q9pip5 homo sapien
7	813.5	45.2	343	1 GP57 HUMAN	Q9pip4 homo sapien
8	782	43.4	338	1 TARI3 RAT	Q923y6 rattus norv
9	743	41.3	348	1 TARI3 HUMAN	Q96ri9 homo sapien
10	741	41.1	333	1 TARI2 RAT	Q923x8 rattus norv
11	733	40.7	344	1 TARI7 RAT	Q923y3 rattus norv
12	732	40.6	345	1 TARI4 RAT	Q923y5 rattus norv
13	731	40.6	344	1 TARI1 RAT	Q923x9 rattus norv
14	730	40.5	344	1 TAI0 RAT	Q923y0 rattus norv
15	722	40.1	358	1 TAI4 RAT	Q923x6 rattus norv
16	722	40.1	358	1 TAI5 RAT	Q923x5 rattus norv
17	715	39.7	345	1 TARI4 HUMAN	Q96ri8 homo sapien
18	713	39.6	358	1 TARI8 RAT	Q923y2 rattus norv
19	710	39.4	358	1 TARI9 RAT	Q923y1 rattus norv
20	704	39.1	358	1 TARI6 RAT	Q923y4 rattus norv
21	696	38.6	342	1 TARI5 HUMAN	Q969n4 homo sapien
22	679	37.7	362	1 TAI3 RAT	Q923x7 rattus norv
23	542.5	30.1	388	1 SH4 CAUPO	Q70528 cavia porce
24	539	29.9	388	1 SH4 MOUSE	P97288 mus musculu
25	534	29.7	388	1 SH4 HUMAN	Q13639 homo sapien
26	529	29.4	406	1 SH4 RAT	Q62758 rattus norv
27	510.5	28.3	459	1 D1DR FUGRU	P53452 fugu rubrip
28	497.5	27.6	465	1 DCDR XENLA	P42291 xenopus lae
29	493.5	27.4	363	1 D1DR CARAU	P35406 carassius a
30	492.5	27.3	358	1 HH2R MOUSE	P97292 mus musculu
31	486	27.0	358	1 HH2R RAT	P25102 rattus norv
32	481	26.7	457	1 DDDR XENLA	P42290 xenopus lae
33	480	26.7	451	1 DADR XENLA	P42289 xenopus lae

RESULT 1	TARI_HUMAN	STANDARD;	PRT;	339 AA.
ID	TARI_HUMAN	STANDARD;	PRT;	339 AA.
AC	Q96RJ0;			
DT	15-MAR-2004 (Rel. 43, Created)			
DT	15-MAR-2004 (Rel. 43, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	Trace amine receptor 1 (TAR-1).			
GN	TARI OR TAL.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21374364; PubMed=11459929;			
RA	Borowsky B., Adham N., Jones K.A., Raddatz R., Artymyshyn R.,			
RA	Ogozalek K.L., Durkin M.M., Lakhani P.P., Bonini J.A., Pathirana S.,			
RA	Boyle N., Pu X., Kouranova E., Lichtblau H., Ochoa F.Y.,			
RA	Branchek T.A., Gerald C.			
RT	"Trace amines: Identification of a family of mammalian G protein-			
RT	coupled receptors."			
RL	Proc. Natl. Acad. Sci. U.S.A. 98:8966-8971(2001).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21580335; PubMed=11723224;			
RA	Bunzow J.R., Sonders M.S., Arttamangkul S., Harrison L.M., Zhang G.,			
RA	Quigley D.I., Darland T., Suchland K.L., Pasumamula S., Kennedy J.L.,			
RA	Olson S.B., Magenis R.E., Amara S.G., Grandy D.K.;			
RT	"Amphetamine, 3,4-methylenedioxymethamphetamine, lysergic acid			
RT	diethylamide, and metabolites of the catecholamine neurotransmitters			
RT	are agonists of a rat trace amine receptor."			
RL	Mol. Pharmacol. 60:1181-1188(2001).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	Kopatz S.A., Aronstam R.S., Sharma S.V.;			
RT	"cDNA clones of human proteins involved in signal transduction			
RT	sequenced (NOV-2002) to the EMBL/GenBank/DBJ databases.			
CC	-!- FUNCTION: Orphan receptor. Could be a receptor for trace amines.			
CC	Activated by endogenous trace amines as well as metabolites of the			
CC	biogenic amine neurotransmitters. Trace amines are biogenic amines			
CC	present in very low levels in mammalian tissues. Although some			
CC	trace amines have clearly defined roles as neurotransmitters in			
CC	invertebrates, the extent to which they function as true			
CC	neurotransmitters in vertebrates has remained speculative. Trace			
CC	amines are likely to be involved in a variety of physiological			
CC	functions that have yet to be fully understood. This receptor			
CC	seems to be mediated by the G(s)-class of G-proteins which			
CC	activate adenylyate cyclase.			
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-!- TISSUE SPECIFICITY: Detected in low levels in discrete regions			
CC	within the central nervous system and in several peripheral			
CC	tissues. Moderately expressed in stomach. Low levels in amygdala,			
CC	kidney, and lung, and small intestine. Trace amounts in cerebellum,			
CC	dorsal root ganglia, hippocampus, hypothalamus, liver, medulla,			

ALIGNMENTS

34	475	26.4	377	1	SH1D_RABIT	P49145 oryctolagus
35	474	26.3	377	1	SH1D_HUMAN	P28221 homo sapien
36	473	26.3	374	1	SH1D_RAT	P28565 rattus norv
37	472.5	26.2	359	1	HH2R_HUMAN	P25021 homo sapien
38	472.5	26.2	359	1	HH2R_PANTR	P60021 pan troglod
39	471	26.2	446	1	DADR_DIDMA	P42288 didelphis m
40	469	26.0	374	1	SH1D_MOUSE	O61224 mus musculu
41	467	25.9	446	1	DADR_PIG	P50130 sus scrofa
42	466.5	25.9	377	1	SH1D_CANFA	P11614 canis famil
43	466.5	25.9	386	1	D1DR_OREMO	P47800 oreochromis
44	462.5	25.7	463	1	D5DR_FUGRU	P53454 fugu rubrip
45	461.5	25.6	376	1	SH1D_CAVPO	Q60484 cavia porce

CC pancreas, pituitary, pontine reticular formation, prostate,
 CC skeletal muscle, and spleen.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -----
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 CC -----
 CC EMBL; AF380185; AAK71236.1; -;
 CC EMBL; AF200627; AAG17112.1; -;
 CC EMBL; AY180374; AAC22154.1; -;
 CC InterPro; IPR000276; GPCR_Rhodopsn.
 CC Pfam; PF00001; 7tm 1; 1.
 CC PRINTS; PR00237; GPCR_RHODOPSN.
 CC PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
 CC PROSITE; PS00262; G_PROTEIN_RECP_F1_2; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family.
 FT DOMAIN 1 25 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 26 46 1 (POTENTIAL).
 FT DOMAIN 47 59 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 60 80 2 (POTENTIAL).
 FT DOMAIN 81 98 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 99 119 3 (POTENTIAL).
 FT DOMAIN 120 136 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 137 157 4 (POTENTIAL).
 FT DOMAIN 158 188 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 189 209 5 (POTENTIAL).
 FT DOMAIN 210 252 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 253 273 6 (POTENTIAL).
 FT DOMAIN 274 287 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 288 308 7 (POTENTIAL).
 FT DOMAIN 309 339 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 96 182 BY SIMILARITY.
 FT CARBOHYD 10 10 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 17 17 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 17 17 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 339 AA; 39091 MW; 5E72FA61CEFA0E0 CRC64;

Query Match 100.0%; Score 1801; DB 1; Length 339;
 Best Local Similarity 100.0%; Pred. No. 8.1e-116;
 Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPFCHNIINISCVKNNWSDVRASLYSLMVLIIITLTVGNLIVIVSISHFKQLHTPTNWL 60
 DB 2 MPFCHNIINISCVKNNWSDVRASLYSLMVLIIITLTVGNLIVIVSISHFKQLHTPTNWL 61
 QY 61 IHSMTAVDFLLGLCLAMPYSMVRSAAHCWYFGEVFCIKHTSTDMLSASIFHLSFISIDR 120
 DB 62 IHSMTAVDFLLGLCLAMPYSMVRSAAHCWYFGEVFCIKHTSTDMLSASIFHLSFISIDR 121
 QY 121 YVAVCDPLRYKAKNNILVICMIFISWSVPVAFAGMIFLELNFKGAEEIYKGVHCRGG 180
 DB 122 YVAVCDPLRYKAKNNILVICMIFISWSVPVAFAGMIFLELNFKGAEEIYKGVHCRGG 181
 QY 181 CSVFFSKISGLVTFMTSPYIPGIMCVYRIYLIKAEQARLISDANQKLGLEMKNGI 240
 DB 182 CSVFFSKISGLVTFMTSPYIPGIMCVYRIYLIKAEQARLISDANQKLGLEMKNGI 241
 QY 241 SOSKERRKAVTKIGIVMGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLWFGYLNSTFNP 300
 DB 242 SOSKERRKAVTKIGIVMGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLWFGYLNSTFNP 301
 QY 301 MYVAFYPPFRKALKMFLGKIFQKDSRCKLFLLESS 338
 DB 302 MYVAFYPPFRKALKMFLGKIFQKDSRCKLFLLESS 339

RESULT 2
 TAR1_MACMU

ID TAR1_MACMU STANDARD; PRT; 338 AA.
 AC Q8HZ64;
 DT 15-MAR-2004 (Rel. 43, Created)
 DT 15-MAR-2004 (Rel. 43, Last sequence update)
 DE Trace amine receptor 1 (Tar-1).
 GN TAR1 OR TAL.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Miller G.M., Madras B.K.;
 RT "Cloning of trace amine receptor 1 (TAR1) from Rhesus monkey.";
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Orphan receptor. Could be a receptor for trace amines.
 CC Activated by endogenous trace amines as well as metabolites of the
 CC biogenic amine neurotransmitters (By similarity). Trace amines are
 CC biogenic amines present in very low levels in mammalian tissues.
 CC Although some trace amines have clearly defined roles as
 CC neurotransmitters in invertebrates, the extent to which they
 CC function as true neurotransmitters in vertebrates has remained
 CC speculative. Trace amines are likely to be involved in a variety
 CC of physiological functions that have yet to be fully understood.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -----
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 CC -----
 CC EMBL; AY13366; AAN06172.1; -;
 CC InterPro; IPR000276; GPCR_Rhodopsn.
 CC Pfam; PF00001; 7tm 1; 1.
 CC PRINTS; PR00237; GPCR_RHODOPSN.
 CC PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
 CC PROSITE; PS00262; G_PROTEIN_RECP_F1_2; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family.
 FT DOMAIN 1 24 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 25 45 1 (POTENTIAL).
 FT DOMAIN 46 58 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 59 79 2 (POTENTIAL).
 FT DOMAIN 80 97 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 98 118 3 (POTENTIAL).
 FT DOMAIN 119 135 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 136 156 4 (POTENTIAL).
 FT DOMAIN 157 187 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 188 208 5 (POTENTIAL).
 FT DOMAIN 209 251 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 252 272 6 (POTENTIAL).
 FT DOMAIN 273 286 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 287 307 7 (POTENTIAL).
 FT DOMAIN 308 338 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 95 181 BY SIMILARITY.
 FT CARBOHYD 9 9 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 16 16 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 338 AA; 38797 MW; 9E7B35456B409B CRC64;
 Query Match 97.6%; Score 1757; DB 1; Length 338;
 Best Local Similarity 96.4%; Pred. No. 7.9e-113;
 Matches 326; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
 QY 1 MPFCHNIINISCVKNNWSDVRASLYSLMVLIIITLTVGNLIVIVSISHFKQLHTPTNWL 60
 DB 1 MPFCHNIINISCVKNNWSDVRASLYSLMVLIIITLTVGNLIVIVSISHFKQLHTPTNWL 60

QY 61 IHSMATVDFLLGCLVMPYSVMSRASHCHWYFGRVFCCKIHTSTDTMLSSASIFHLSFISIDR 120
 Db 61 IHSMATVDFLLGCLVMPYSVMSRASHCHWYFGRVFCCKIHTSTDTMLSSASIFHLSFISIDR 120
 QY 121 YVAVCDPLRYKAKMILVICVMIFISWSVPVAFAGMIFLELNFKGABEIIYKHVHCRCGG 180
 Db 121 YVAVCDPLRYKAKMILVICVMIFISWSVPVAFAGMIFLELNFKGABEIIYKHVHCRCGG 180
 QY 181 CSVFPSKISGVLTFTMTSPYIPGSMILCVYRIYLIYIAKQARLISDANOKLQIGLEMKNGI 240
 Db 181 CSVFPSKISGVLTFTMTSPYIPGSMILCVYRIYLIYIAKQARLISDANOKLQIGLEMKNGI 240
 QY 241 SOSKERKAVKTLGIYVGMVFLICWCPEFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTNP 300
 Db 241 SOSKERKAVKTLGIYVGMVFLICWCPEFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTNP 300
 QY 301 MYAFYFYPFRKALOMLFGKIFQKDSRCKLFLLESS 338
 Db 301 MYAFYFYPFRKALOMLFGKIFQKDSRCKLFLLESS 338
 RESULT 3
 TARI RAT
 ID TARI RAT STANDARD; PRT; 332 AA.
 AC Q92379; O8VHQ5;
 DT 15-MAR-2004 (Rel. 43, Created)
 DT 15-MAR-2004 (Rel. 43, Last sequence update)
 DE Trace amine receptor 1 (Tar-1).
 GN TARI OR TAL.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A., AND VARIANT GLN-170.
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=21374364; PubMed=11459929;
 RA Borowsky B., Adham N., Jones K.A., Raddatz R., Artymyshyn R.,
 RA Ogozalek K.L., Durkin M.M., Lakhlani P.P., Bonini J.A., Pathirana S.,
 RA Boyle N., Pu X., Kouranova E., Lichtblau H., Ochoa F.Y.,
 RA Branchek T.A., Gerald C.;
 RA "Trace amines: Identification of a family of mammalian G protein-
 coupled receptors.";
 RT Proc. Natl. Acad. Sci. U.S.A. 98:8966-8971 (2001).
 RL [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Cerebellum, and Pancreatic tumor;
 RX MEDLINE=21580235; PubMed=11723224;
 RA Bunzow J.R., Sonders M.S., Artamangkul S., Harrison L.M., Zhang G.,
 RA Quigley D.I., Darland T., Suchland K.B., Pasumamula S., Kennedy J.L.,
 RA Olson S.B., Magenis R.E., Anara S.G., Grandy D.K.;
 RA "Amphetamine, 3,4-methylenedioxymethamphetamine, lysergic acid
 diethylamide, and metabolites of the catecholamine neurotransmitters
 are agonists of a rat trace amine receptor.";
 RL Mol. Pharmacol. 60:1181-1188 (2001).
 CC -!- FUNCTION: Orphan receptor. Could be a receptor for trace amines.
 CC Activated by endogenous trace amines as well as metabolites of the
 CC biogenic amine neurotransmitters. Trace amines are biogenic amines
 CC present in very low levels in mammalian tissues. Although some
 CC trace amines have clearly defined roles as neurotransmitters in
 CC invertebrates, the extent to which they function as true
 CC neurotransmitters in vertebrates has remained speculative. Trace
 CC amines are likely to be involved in a variety of physiological
 CC functions that have yet to be fully understood. This receptor
 CC seems to be mediated by the G(s)-class of G-proteins which
 CC activate adenylate cyclase.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Widely distributed, but in low abundance,
 CC throughout the brain. Highest levels detected in the olfactory
 CC bulb, nucleus accumbens/olfactory tubercle, prefrontal cortex and
 CC other cortical regions, midbrain regions consisting of substantia
 CC nigra and ventral tegmentum, cerebellum, and pons/medulla. Among

peripheral tissues, highest level observed in the liver, less
 expression in kidney, gastrointestinal tract, spleen, pancreas,
 and heart.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 CC
 CC EMBL; AF380186; AAK71237.1; --
 CC EMBL; AF421352; AAL65137.1; --
 CC Pfam; PF00001; 7tm.1; 1.
 CC PRINTS; PR00237; GPCRHHODOPS.
 CC PROSITE; PS00237; G-PROTEIN RECEPTOR F1_1; 1.
 CC PROSITE; PS00262; G-PROTEIN RECEPTOR F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family; Polymorphism.
 FT DOMAIN 1 24 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 25 45 1 (POTENTIAL).
 FT DOMAIN 46 58 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 59 79 2 (POTENTIAL).
 FT DOMAIN 80 97 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 98 118 3 (POTENTIAL).
 FT DOMAIN 119 138 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 139 159 4 (POTENTIAL).
 FT DOMAIN 160 187 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 188 208 5 (POTENTIAL).
 FT DOMAIN 209 249 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 250 270 6 (POTENTIAL).
 FT DOMAIN 271 287 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 288 308 7 (POTENTIAL).
 FT DOMAIN 309 332 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 95 181 BY SIMILARITY.
 FT CARBOHYD 9 9 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 16 16 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 283 283 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT VARIANT 170 170 L -> Q.
 SQ SEQUENCE 332 AA; 38021 MW; AD7F3A728C77B246 CRC64;
 Query Match 77.9%; Score 1403; DB 1; Length 332;
 Best Local Similarity 78.1%; Pred. No. 8.9e-89;
 Matches 261; Conservative 27; Mismatches 44; Indels 2; Gaps 1;
 QY 1 MPFCHNIINISCVKNWSDVRASLYSLMWLILITLVGNLIVIVISHSFKQLHTPTNWL 60
 Db 1 MHLCHNSANISHTNSWSDVRASLYSLILITLVGNLIVIVISHSFKQLHTPTNWL 60
 QY 61 IHSMATVDFLLGCLVMPYSVMSRASHCHWYFGRVFCCKIHTSTDTMLSSASIFHLSFISIDR 120
 Db 61 LHSMAVDFLLGCLVMPYSVMSRASHCHWYFGRVFCCKIHTSTDTMLSSASIFHLSFISIDR 120
 QY 121 YVAVCDPLRYKAKMILVICVMIFISWSVPVAFAGMIFLELNFKGABEIIYKHVHCRCGG 180
 Db 121 YVAVCDPLRYKAKMILVICVMIFISWSVPVAFAGMIFLELNFKGABEIIYKHVHCRCGG 180
 QY 181 CSVFPSKISGVLTFTMTSPYIPGSMILCVYRIYLIYIAKQARLISDANOKLQIGLEMKNGI 240
 Db 181 CSVFPSKISGVLTFTMTSPYIPGSMILCVYRIYLIYIAKQARLISDANOKLQIGLEMKNGI 240
 QY 241 SOSKERKAVKTLGIYVGMVFLICWCPEFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTNP 300
 Db 241 SOSKERKAVKTLGIYVGMVFLICWCPEFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTNP 300
 QY 301 MYAFYFYPFRKALOMLFGKIFQKDSRCKLFL 334
 Db 299 MYAFYFYPFRKALOMLFGKIFQKDSRCKLFL 332

RESULT 4
TAR1_MOUSE
ID TAR1_MOUSE STANDARD; PRT; 332 AA.
AC Q923Y8;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Trace amine receptor 1 (Tar-1).
GN TAR1 OR TA1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RX MEDLINE=21374364; PubMed=11459929;
RA Borowsky B., Adham N., Jones K.A., Raddatz R., Artymyshyn R.,
RA Ogorzalek K.L., Durkin M.M., Lakhani P.P., Bonini J.A., Pathirana S.,
RA Boyle N., Pu X., Kouranova E., Lichtblau H., Ochoa F.Y.,
RA Brancheck T.A., Gerald C.;
RT "Trace amines: Identification of a family of mammalian G protein-
coupled receptors.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:8966-8971(2001).
CC -!- FUNCTION: Orphan receptor. Could be a receptor for trace amines.
CC Activated by endogenous trace amines as well as metabolites of the
CC biogenic amine neurotransmitters (By similarity). Trace amines are
CC biogenic amines present in very low levels in mammalian tissues.
CC Although some trace amines have clearly defined roles as
CC neurotransmitters in invertebrates, the extent to which they
CC function as true neurotransmitters in vertebrates has remained
CC speculative. Trace amines are likely to be involved in a variety
CC of physiological functions that have yet to be fully understood.
CC This receptor seems to be mediated by the G(s)-class of G-proteins
CC which activate adenylate cyclase (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Widely distributed throughout the brain.
CC Strongly expressed in the mitral cell layer of the olfactory bulb,
CC piriform cortex, the arcuate, motor, and mesencephalic trigeminal
CC nuclei, lateral reticular and hypoglossal nuclei, cerebellar
CC Purkinje cells, and ventral horn of the spinal cord. Moderately
CC expressed in the frontal, entorhinal, and agranular cortices, the
CC ventral pallidum, thalamus, hippocampus, several hypothalamic
CC nuclei, ambiguous, dorsal raphe, and gigantocellular reticular
CC nuclei. Weakly expressed in the septum, basal ganglia, amygdala,
CC myelencephalon, and spinal cord dorsal horn. Particularly
CC interesting is the moderate expression in several monoaminergic
CC cell groups, namely the dorsal raphe, the locus coeruleus, and the
CC ventral tegmental area.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF380187; AAK71238.1; -.
CC MGD; MGI:2148258; Tar1.
CC GO; GO:0016021; C:integral to membrane; IC.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCRHOODPSN.
CC PROSITE; PS00237; G-PROTEIN RECEPT_F1_1; 1.
CC PROSITE; PS0262; G-PROTEIN RECEPT_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein;
CC Multigene family.
CC DOMAIN 1 24 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 25 45 1 (POTENTIAL).
CC FT DOMAIN 46 58 CYTOPLASMIC (POTENTIAL).
CC FT 59 79 2 (POTENTIAL).
CC FT

FT DOMAIN 80 97 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 98 118 3 (POTENTIAL).
FT DOMAIN 119 138 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 139 159 4 (POTENTIAL).
FT DOMAIN 160 187 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 188 208 5 (POTENTIAL).
FT DOMAIN 209 249 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 250 270 6 (POTENTIAL).
FT DOMAIN 271 287 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 288 308 7 (POTENTIAL).
FT DOMAIN 309 332 CYTOPLASMIC (POTENTIAL).
FT DISULFID 95 181 BY SIMILARITY.
FT CARBOHYD 9 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 332 AA; 37620 MW; 580BE692B1892264 CRC64;
Query Match 75.0%; Score 1351; DB 1; Length 332;
Best Local Similarity 75.4%; Pred. No. 3e-85;
Matches 252; Conservative 31; Mismatches 49; Indels 2; Gaps 1;
QY 1 MPFCHNINISCVKNNWSDVRASLYSLMVLIIITLVGNLIVIVYISHFKQLHTPTNWL 60
Db 1 MHLCHAITNISHRNSDWSREVQASLYSLMLIATLVGNLIVIVISISHFKQLHTPTNWL 60
QY 61 IHSMATVDFLLGCLVMPYSMVRSACHYFGEVFCVCKIHTSTDIMLSSASIFHLFSIDR 120
Db 61 LHSMAIVDFLLGCLIMPCSMVATVERCWYFGBILCKVHTSTDIMLSSASIFHLAFISIDR 120
QY 121 YVACDPLRYKAKINILVTCVMIFISWSVPAVAFGMFLFNFGAEEIYKHKHCRGG 180
Db 121 YVACDPLRYKAKINISTILVMILVSWSLPVAVAFGMFLFNFGAEEIYKHKHCRGG 180
QY 181 CSVFESKISGLVTWTSFVPGSIMLCVYRYLYLAKQARLISDANOKLOIGLEMKNGI 240
Db 181 CSPFESKISGLVLAFTSFYIPGSMVLFVYRYLYLAKQARLISDANOKLOIGLEMKNGI 240
QY 241 SOSKERKAVKTLGIVMGVFLICWCFFICTVMDPFLHPIPTLNDVLVFWGLNSTENP 300
Db 239 PQSKETKAAKTLGIVMGVFLVWCFFICTVLDPLGVIPPSINDALYFWGLNSALNP 298
QY 301 MYVAFYFWRKALQKMLFGKIFQKDSRCKLFL 334
Db 299 MYVAFYFWRKALQKMLFGKIFQKDSRCKLFL 332
RESULT 5
TAR2_RAT
ID TAR2_RAT STANDARD; PRT; 347 AA.
AC Q923Y7;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Trace amine receptor 2 (Tar-2).
GN TAR2 OR TA2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=21374364; PubMed=11459929;
RA Borowsky B., Adham N., Jones K.A., Raddatz R., Artymyshyn R.,
RA Ogorzalek K.L., Durkin M.M., Lakhani P.P., Bonini J.A., Pathirana S.,
RA Boyle N., Pu X., Kouranova E., Lichtblau H., Ochoa F.Y.,
RA Brancheck T.A., Gerald C.;
RT "Trace amines: Identification of a family of mammalian G protein-
coupled receptors.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:8966-8971(2001).
CC -!- FUNCTION: Orphan receptor. Could be a receptor for trace amines.
CC Of the biogenic trace amine tested, activated only by beta-
CC phenylethylamine (beta-PEA) and tryptamine; however, the response
CC is of low potency. Trace amines are biogenic amines present in
CC very low levels in mammalian tissues. Although some trace amines


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QY 85 EHCWTFGEVCKIHTSDIMLSASIFHLFSISIDRYAVVCDPLRYKAKMNLIVCMVLP 144
Db 61 ENCWFGLTFCKIYYSFDLMLTSISFLHCSVAIDRFYAICVPLLYSTKITIPVIRKILL 120
QY 145 ISWSVPAVAFGMIFUENLNFKAEEIYYKHVHCRGCVFFSKISGVLTFMTSFFYIPGSI 204
Db 121 LCWSVPGAFAVGAFAVSEAVADGIEG-YDILVACSSCPVFNKLMGTTLFMAGFFTPGSM 179
QY 205 MLCVYVRIYLLAKEQARLLSD--ANQKLIQIGLEKNGISQSKERKAVKTLGIVMGVFLIC 262
Db 180 MVIYIKFAVGRKKHAHANN--RENQNNQV-----KKDKAAKTLGIVGVFLIC 229
QY 263 WCPFFICTVMDPLHVIIPPTLNDVLWFCYLNSTENPMVYAFFYFWRKAKMMLFGKI 322
Db 230 WPCPFTILLDFLNESTPVLFDALTWFGYFNSTCNPLIYGFYFWRFRALKYILLGKI 289
QY 323 F-----QKDS 327
Db 290 FSSCFHNTILCMQKES 305

RESULT 7
GP57_HUMAN
ID GP57_HUMAN STANDARD; PRT; 343 AA.
AC Q9P1P4;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Probable G protein-coupled receptor GPR57.
GN GPR57.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20149852; PubMed=10684976;
RA Lee D.K., Lynch K.R., Nguyen T., Im D.-S., Cheng R., Saldivia V.R.,
RA Liu Y., Liu I.S.C., Heng H.H.Q., Seeman P., George S.R., O'Dowd B.F.,
RA Marchese A.;
RT Cloning and characterization of additional members of the G protein-
RT coupled receptor family."
RL Biochim. Biophys. Acta 1490:311-323 (2000).
CC -!- FUNCTION: Orphan receptor.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Not expressed in the pons, thalamus, globus
CC pallidus, caudate, putamen or cerebellum.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL; AF112461; AAF27279.1; -.
DR Genbank; HGNC:4513; GPR57.
DR MIM; 604848; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 35 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 36 56 1 (POTENTIAL).
FT DOMAIN 57 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 150 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 151 168 3 (POTENTIAL).
FT DOMAIN 169 172 CYTOPLASMIC (POTENTIAL).

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FT TRANSMEM 173 193 4 (POTENTIAL).
FT DOMAIN 194 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 223 5 (POTENTIAL).
FT DOMAIN 224 257 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 258 278 6 (POTENTIAL).
FT DOMAIN 279 287 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 288 308 7 (POTENTIAL).
FT DOMAIN 309 343 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 145 145 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 343 AA; 39065 MW; DC513D15ABBC026F CRC64;

Query Match 45.2%; Score 813.5; DB 1; Length 343;
Best Local Similarity 46.0%; Pred. No. 1.1e-48;
Matches 159; Conservative 57; Mismatches 99; Indels 31; Gaps 5;

QY 4 CHNIN-----ISCVKNN-----WSNDVRASLYSLMVLIIITLTVGNLIVIVSISH 49
Db 13 CPKFNKILSSHQPLFSCPGDNVFGYDWSHDY-----PLFGLNIVIMVISH 58
QY 50 FKQLHTPTNMLIHSMTATVDFLLGCLVMPYSMSVRSABHCWYFGEVFCCKIHTSDIMLSAS 109
Db 59 FKQLHSPTNFLILSMATTDLLGLGVIMPYSIMRSVESCWYFGDGCKFHTSDIMLRLTS 118
QY 110 IFHLFSISIDRYAVVCDPLRYKAKMNLIVCMVIFISWSVPAVFAFGMIFLELNFKGAE 169
Db 119 IFHLCSIAIDRYAVVCDPLRYKAKMNLIVCMVIFISWSVPAVFAFGMIFLELNFKGAE 178
QY 170 IYKHVHCRGCVFFSKISGVLTFMTSFPYIPGSMICVYIYIYIAKQOARLISDANQK 229
Db 179 -YKILVACFNFCALTFFKFWGTILFTTCFFTPGSMVGIYKIFIVSKQHARVISHPEN 237
QY 230 LQIGLEKNGISQSKERKAVKTLGIVMGVFLICWCPFFICTVMDPLHVIIPPTLNDVLI 289
Db 238 TKGA--VKHLSKKDKRKAATLGIWGVFLACWUPLFLAVLIDPVLDTSTLILDLIV 295
QY 290 WFGYLNSTENPMVYAFFYFWRKAKMMLFGKIFQKDSRCKDLFE 335
Db 296 WLRYFNSTCNPLIHGFFNFWQKAFKIVSGKIFSSHSETANLFE 341

RESULT 8
TAR3_RAT
ID TAR3_RAT STANDARD; PRT; 338 AA.
AC Q923Y6;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Trace amine receptor 3 (Tar-3).
GN TAR3 OR TA3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=21374364; PubMed=11459929;
RA Borowsky B., Adham N., Jones K.A., Raddatz R., Artymyshyn R.,
RA Ogozalek K.L., Durkin M.M., Lakhani P.P., Bonini J.A., Pathirana S.,
RA Boyle N., Pu X., Kouranova E., Lichtblau H., Ochoa F.Y.,
RA Branchek T.A., Gerald C.;
RT "Trace amines: Identification of a family of mammalian G protein-
RT coupled receptors."
RL Proc. Natl. Acad. Sci. U.S.A. 98:8966-8971 (2001).
CC -!- FUNCTION: Orphan receptor. Could be a receptor for trace amines.
CC Trace amines are biogenic amines present in very low levels in
CC mammalian tissues. Although some trace amines have clearly defined
CC roles as neurotransmitters in invertebrates, the extent to which
CC they function as true neurotransmitters in vertebrates has
CC remained speculative. Trace amines are likely to be involved in a
CC variety of physiological functions that have yet to be fully
CC understood.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

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QY 4 CHNIINISCVKNWNSDVASLSYSLMVLIIITLVGNLIVIVSISHFKQLHTPTNWLHIS 63
DB 14 CYVNVESICKTPYSGPRSSIIYAVLGVGAVLAAGNLLMIAILHFKQLHTPTNPLIAS 73
QY 64 MATVDLFLGCLVMPYSWVSABHCHWYGVFCIKHTSTDIMLSSASIFHLSPISIDRYVA 123
DB 74 LACADFLVGVTPWPFSTVRSVSVSGYSGYKFKHTCFDTSFCFASLFLHLCISVDRYTA 133
QY 124 VCDPLRYKAKMNLIVICVMIFISWSVPAVFAFGMIFLEINFGABBIYKHVHCRCGCVS 183
DB 134 VTDPLTYPTKFTVSVSGICIVLSWFFSVTYSFIFVTGANEEGIEBLVVA-LTCVGGCOA 192
QY 184 PFSKISGVLTFWTSFVIPSIMLCVYRIYLAKQARLISDANKQLQIGLEMKNGISQS 243
DB 193 PLNQWVLLCFLL-FEIPNVAVFYISKIFLVAQQAQKIESTASQAQSSSYKERVAK 251
QY 244 KERKAVKTLGIYMGVFLICWCPCFFICTVMDPPLHYIIPPLNDVLIVFGYLNSTENPMVY 303
DB 252 RERKAATLGIAMAAFLVSWLPYLVDAVIDAYMNFITPPYVVEILLVWCYVYNSAMNPLIY 311
QY 304 AFYFYPFRKAKMMLFGKIFQKDSRCKLFLE 335
DB 312 AFYQWFGKAIKLIYSGKVLRTDSTTNLFSE 343
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RESULT 10
TAR7 RAT
ID TAR7 RAT STANDARD; PRT; 333 AA.
AC Q923X8;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DE Trace amine receptor 12 (Tar-12).
GN TAR12 OR TAR12.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=21374364; PubMed=11459929;
RA Borowsky B., Adham N., Jones K.A., Raddatz R., Artymyshyn R.;
BA Ogozalek K.L., Durkin M.M., Lakhiani P.P., Bonini J.A., Pathirana S.,
BO Boyle N., Pu X., Kouranova E., Lichtblau H., Ochoa F.Y.,
RA Branchek T.A., Gerald C.;
RT "Trace amines: Identification of a family of mammalian G protein-
coupled receptors.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:8966-8971 (2001).
CC -!- FUNCTION: Orphan receptor. Could be a receptor for trace amines.
CC Trace amines are biogenic amines present in very low levels in
CC mammalian tissues. Although some trace amines have clearly defined
CC roles as neurotransmitters in invertebrates, the extent to which
CC they function as true neurotransmitters in vertebrates has
CC remained speculative. Trace amines are likely to be involved in a
CC variety of physiological functions that have yet to be fully
CC understood.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -----
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CC -----
CC EMBL; AF380200; AAK71251.1; -.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
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DR PROSITE; PS00237; G PROTEIN RECEPTOR F1.1; 1.
DR PROSITE; PS00262; G PROTEIN RECEPTOR F1.2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family.
FT DOMAIN 1 22 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 23 43 1 (POTENTIAL).
FT DOMAIN 44 58 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 59 79 2 (POTENTIAL).
FT DOMAIN 80 99 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 100 118 3 (POTENTIAL).
FT DOMAIN 119 141 4 (POTENTIAL).
FT TRANSMEM 142 162 4 (POTENTIAL).
FT DOMAIN 163 186 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 187 207 5 (POTENTIAL).
FT TRANSMEM 208 249 6 (POTENTIAL).
FT DOMAIN 250 271 7 (POTENTIAL).
FT TRANSMEM 271 283 7 (POTENTIAL).
FT DOMAIN 284 304 7 (POTENTIAL).
FT TRANSMEM 305 333 7 (POTENTIAL).
FT DISULFID 95 180 BY SIMILARITY.
FT CARBOHYD 9 N-LINKED (GLCNAC... (POTENTIAL).
SQ SEQUENCE 333 AA; 37467 MW; 65BD886131C1C85B CRC64;
Query Match 41.1%; Score 741; DB 1; Length 333;
Best Local Similarity 41.8%; Pred. No. 8.7e-44;
Matches 140; Conservative 70; Mismatches 123; Indels 2; Gaps 2;
QY 1 MPFCNINISCVKNWNSDVASLSYSLMVLIIITLVGNLIVIVSISHFKQLHTPTNWL 60
DB 1 MOLCYEKLNRSCVRSPYSGPRLLIYAVFGAVLAAGNLLMIAILHFKQLHSPANFL 60
QY 61 IHSMATVDLFLGCLVMPYSWVSABHCHWYGVFCIKHTSTDIMLSSASIFHLSPISIDR 120
DB 61 VASLACADFLVGLTVNPFWSVSGVCGWYFGDIYCKFHSSFDGSCYCSIFHLCLFISADR 120
QY 121 YVAVCDPLRYKAKMNLIVICVMIFISWSVPAVFAFGMIFLEINFGABBIYKHVHCRCG 180
DB 121 YVAVSDPLIYPRFTASVSGKCIITFSWLLSIYVSFLVTVGNEAGLEDL-VSALTCVSG 179
QY 181 CSVFFSKISGVLTFWTSFVIPSIMLCVYRIYLAKQARLISDANKQLQIGLEMKNGI 240
DB 180 CQIAVNSQWVFINFLL-FLVPALVNMVTVYSKIFLIAKQAOAIEKMGKQTARASYSKDR 238
QY 241 SQSKERKAVKTLGIYMGVFLICWCPCFFICTVMDPPLHYIIPPLNDVLIVFGYLNSTENP 300
DB 239 VAKRERKAATLGIAMAAFLVSWLPYLVDAVIDAYMNFITPPYVVEILLVWCYVYNSAMNP 298
QY 301 MYAFYFYPFRKAKMMLFGKIFQKDSRCKLFLE 335
DB 299 LIYAFYFYPFRKAKIILVITGKILRENSATNLFPE 333
RESULT 11
TAR7 RAT
ID TAR7 RAT STANDARD; PRT; 344 AA.
AC Q923Y3;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DE Trace amine receptor 7 (Tar-7).
GN TAR7 OR TAR7.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=21374364; PubMed=11459929;
RA Borowsky B., Adham N., Jones K.A., Raddatz R., Artymyshyn R.;
BA Ogozalek K.L., Durkin M.M., Lakhiani P.P., Bonini J.A., Pathirana S.,
BO Boyle N., Pu X., Kouranova E., Lichtblau H., Ochoa F.Y.,
RA Branchek T.A., Gerald C.;
```



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RP SEQUENCE FROM N.A.
RC STRAIN-Sprague-Dawley;
RA MEDLINE=21374364; PubMed=11459929;
RA Borowsky B., Adham N., Jones K.A., Raddatz R., Artymyshyn R.,
RA Ogozalek K.L., Durkin M.M., Lakhani P.P., Bonini J.A., Pathirana S.,
RA Boyle N., Pu X., Kouranova E., Lichtblau H., Ochoa F.Y.,
RA Brancheck T.A., Gerald C.;
RT "Trace amines: Identification of a family of mammalian G protein-
RT coupled receptors.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:8966-8971(2001).
CC -!- FUNCTION: Orphan receptor. Could be a receptor for trace amines.
CC Trace amines are biogenic amines present in very low levels in
CC mammalian tissues. Although some trace amines have clearly defined
CC roles as neurotransmitters in invertebrates, the extent to which
CC they function as true neurotransmitters in vertebrates has
CC remained speculative. Trace amines are likely to be involved in a
CC variety of physiological functions that have yet to be fully
CC understood.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC -----
CC EMBL; AF380198; AAK71249.1; -.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm1.1.
CC PRINTS; PR00237; GPCRHHODOPSN.
CC PROSITE; PS00237; G-PROTEIN RECEPT_F1_1; 1.
CC PROSITE; PS0262; G-PROTEIN RECEPT_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein;
CC Multigene family.
CC DOMAIN 1 36 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 37 57 1 (POTENTIAL).
CC DOMAIN 58 67 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 68 88 2 (POTENTIAL).
CC DOMAIN 89 102 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 103 127 3 (POTENTIAL).
CC DOMAIN 128 146 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 147 167 4 (POTENTIAL).
CC DOMAIN 168 196 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 197 217 5 (POTENTIAL).
CC DOMAIN 218 260 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 261 281 6 (POTENTIAL).
CC DOMAIN 282 295 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 296 319 7 (POTENTIAL).
CC DOMAIN 320 344 CYTOPLASMIC (POTENTIAL).
CC DISULFID 96 189 BY SIMILARITY.
CC CARBOHYD 4 4 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 18 18 N-LINKED (GLCNAC. .) (POTENTIAL).
CC SEQUENCE 344 AA; 38015 MW; 6AB7A52CE3BEB92 CRC64;
CC
CC Query Match 40.5%; Score 730; DB 1; Length 344;
CC Best Local Similarity 41.2%; Pred. No. Se-43;
CC Matches 139; Conservative 71; Mismatches 123; Indels 4; Gaps 3;
CC
CC QY 1 MPFCHNINISCVKNWSDVRASLYSLMVLILITLVGNLVIVISHSFKOLHTPTWNL 60
CC Db 10 LQLCYENVNASCITKTPSPGLVLLYMWFGGAVLAVCGNLLVLSVLHFKQLHSPANFL 69
CC
CC QY 61 IHSMATVDFLLGLVMPYSWMSABCHWYFGVFCIKHTSDIMLSSASIFHLSISIDR 120
CC Db 70 IASLASADFLVIGISWMPFSWMSIESCWYFGTFCSLHSCCDVAFCYSALHLCISVDR 129
CC
CC QY 121 YVAVCDPLRYKAKMILVICVMIFTSWSVPVAFVAFGMIFLENFKABEIIYKHHVCRGG 180
CC Db 130 YVAVTDPLVYPTKFTVSVSGICISISWILPLVYSSAVFVTGTISAMGIENL-VSALNCVGG 188

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QY 181 CSVFESKISGVLTFTMTSFVIPGIMLCVYRYIYLTAKEQARLI--SDANQKLIQIGLEMKN 238
Db 189 CQVVNVNQDWLISFL--FFIPTLVMIILYSKIFLVAKQAVKIETSVSGSKGESSLESKH 247
QY 239 GISQSKERKAVKTLGIWVGVLICWPFPCFFICWMDPFFLHIIPTLNDVLINFGYLNSTF 298
Db 248 ARVAKRERKAAKTLGTVLAFIVSLWPTIDILDAFMGFTIPAYVVEFCSSAYNSAM 307
QY 299 NPMVTAFYPPWPRKALKMMLFKQIFQKDSRSRCKLFLE 335
Db 308 NPLIYAFYPPWPRKAMKILSGKILKGHSSTTSLESE 344

RESULT 15
TAl4 RAT
ID TAl4 RAT STANDARD; PRT; 358 AA.
AC Q923X6;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Trace amine receptor 14 (Tar-14).
GN TARI4 OR TAl4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Sprague-Dawley;
RX MEDLINE=21374364; PubMed=11459929;
RA Borowsky B., Adham N., Jones K.A., Raddatz R., Artymyshyn R.,
RA Ogozalek K.L., Durkin M.M., Lakhani P.P., Bonini J.A., Pathirana S.,
RA Boyle N., Pu X., Kouranova E., Lichtblau H., Ochoa F.Y.,
RA Brancheck T.A., Gerald C.;
RT "Trace amines: Identification of a family of mammalian G protein-
RT coupled receptors.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:8966-8971(2001).
CC -!- FUNCTION: Orphan receptor. Could be a receptor for trace amines.
CC Trace amines are biogenic amines present in very low levels in
CC mammalian tissues. Although some trace amines have clearly defined
CC roles as neurotransmitters in invertebrates, the extent to which
CC they function as true neurotransmitters in vertebrates has
CC remained speculative. Trace amines are likely to be involved in a
CC variety of physiological functions that have yet to be fully
CC understood.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; AF380202; AAK71253.1; -.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm1.1.
CC PRINTS; PR00237; GPCRHHODOPSN.
CC PROSITE; PS00237; G-PROTEIN RECEPT_F1_1; 1.
CC PROSITE; PS0262; G-PROTEIN RECEPT_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein;
CC Multigene family.
CC DOMAIN 1 47 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 48 68 1 (POTENTIAL).
CC DOMAIN 69 83 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 84 104 2 (POTENTIAL).
CC DOMAIN 105 121 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 122 143 3 (POTENTIAL).
CC DOMAIN 144 166 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 167 187 4 (POTENTIAL).
CC DOMAIN 188 212 EXTRACELLULAR (POTENTIAL).

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 8, 2004, 10:16:35 ; Search time 44 Seconds

(without alignments)
2423.753 Million cell updates/sec

Title: US-09-633-145-2

Perfect score: 1801

Sequence: 1 MPFCHNIINISCKVNSND.....FGKIFQDSSRCKLFLELSS 338

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriap:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1801	100.0	339	4	Q96RJ0	Q96rj0 homo sapien
2	1757	97.6	338	6	Q8HZ64	Q8hz64 macaca mula
3	1403	77.9	332	11	Q923Y9	Q923y9 rattus norv
4	1398	77.6	332	11	Q8VH05	Q8vhq5 rattus norv
5	1351	75.0	332	11	Q923Y8	Q923y8 mus musculu
6	927.5	51.5	347	11	Q923Y7	Q923y7 rattus norv
7	815	45.3	306	4	Q9P1P5	Q9p1p5 homo sapien
8	813.5	45.2	343	4	Q9P1P4	Q9p1p4 homo sapien
9	782	43.4	338	11	Q923Y6	Q923y6 rattus norv
10	743	41.3	348	4	Q96R19	Q96r19 homo sapien
11	741	41.1	333	11	Q923X8	Q923x8 rattus norv
12	733	40.7	344	11	Q923Y3	Q923y3 rattus norv
13	732	40.6	345	11	Q923Y5	Q923y5 rattus norv
14	731	40.6	374	11	Q923X9	Q923x9 rattus norv
15	730	40.5	344	11	Q923Y0	Q923y0 rattus norv
16	722	40.1	358	11	Q923X6	Q923x6 rattus norv

17	722	40.1	358	11	Q923X5	Q923x5 rattus norv
18	715	39.7	345	4	Q96R18	Q96r18 homo sapien
19	713	39.6	358	11	Q923Y2	Q923y2 rattus norv
20	710	39.4	358	11	Q923Y1	Q923y1 rattus norv
21	704	39.1	358	11	Q923Y4	Q923y4 rattus norv
22	679	37.7	362	11	Q923X7	Q923x7 rattus norv
23	677.5	37.6	337	4	O14804	O14804 homo sapien
24	580.5	32.2	352	13	Q9YHY4	Q9yhy4 lampetra fl
25	545.5	30.3	328	13	Q9YHV8	Q9yvh8 figu rubrip
26	534	29.7	387	4	Q96K10	Q96k10 homo sapien
27	534	29.7	388	4	Q8IXH9	Q8ixh9 homo sapien
28	526.5	29.2	328	13	Q9YHV7	Q9yvh7 figu rubrip
29	511	28.4	353	13	Q9YHY3	Q9yhy3 lampetra fl
30	503	27.9	446	13	O42315	O42315 cyprinus ca
31	498.5	27.7	445	13	Q98842	Q98842 anguilla an
32	495	27.5	437	13	O42316	O42316 cyprinus ca
33	488.5	27.1	358	11	Q9QX37	Q9qx37 mus musculu
34	488.5	27.1	397	11	Q9D282	Q9d282 mus musculu
35	488.5	27.1	445	13	Q98841	Q98841 anguilla an
36	481	26.7	448	13	Q98844	Q98844 anguilla an
37	477	26.5	508	5	Q9VCZ3	Q9vcz3 drosophila
38	476.5	26.5	458	13	Q98843	Q98843 anguilla an
39	473	26.3	374	11	Q8BUW7	Q8buw7 mus musculu
40	472.5	26.2	391	5	O96716	O96716 branchiosto
41	472.5	26.2	397	4	O7Z5R9	O7z5r9 homo sapien
42	464	25.8	446	6	Q8WND7	Q8wnd7 bos taurus
43	462	25.7	394	5	Q9NHF3	Q9nhf3 aplysia cal
44	461	25.6	394	5	Q9NJS6	Q9njs6 aplysia kur
45	459	25.5	377	6	Q9N263	Q9n263 sus scrofa

ALIGNMENTS

RESULT 1

Q96RJ0 ID Q96RJ0 PRELIMINARY; PRT; 339 AA.
AC Q96RJ0;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Trace amine receptor 1 (Putative catecholamine receptor).
GN TAL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21374364; PubMed=11459929;
RA Borowsky B., Adham N., Jones K.A., Raddatz R., Artymyshyn R.,
RA Ogozalek K.L., Durkin M.M., Iakhlani P.P., Bonini J.A., Pathirana S.,
RA Boyle N., Pu X., Kouranova E., Lichtblau H., Ochoa F.Y.,
RA Brancheck T.A., Gerald C.;
RT "Trace amines: Identification of a family of mammalian G protein-
coupled receptors.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:8966-8971(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21580235; PubMed=11723224;
RA Bunzow J.R., Sonders M.S., Arttamangkul S., Harrison L.M., Zhang G.,
RA Quigley D.I., Darland T., Suchland K.L., Pasumamula S., Kennedy J.L.,
RA Olson S.B., Magenis R.E., Amara S.G., Grandy D.K.;
RT "Amphetamine, 3,4-methylenedioxymethamphetamine, lysergic acid
diethylamide, and metabolites of the catecholamine neurotransmitters
are agonists of a rat trace amine receptor.";
RL Mol. Pharmacol. 60:1181-1188(2001).
RN [3]
RP SEQUENCE FROM N.A.
RA Kopatz S.A., Aronstam R.S., Sharma S.V.;
RT "Isolation of cDNA coding for Human Trace Amine Receptor (TAR)1.";
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
CC 1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

```

CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AF380185; AAK71236.1; -.
DR EMBL; AF200627; AAG17112.1; -.
DR EMBL; AY180374; AAO22154.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR F1.1; 1.
DR PROSITE; PS0262; G-PROTEIN RECEPTOR F1.2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 339 AA; 39091 MW; 5E72FA61CEFA0E0 CRC64;

Query Match 100.0%; Score 1801; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.4e-159;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPFCHNIINISCVKNWNSDVRSIYSLMWLIILITLVGNLIVIVISISHFKQLHTPTNWL 60
DB 2 MPFCHNIINISCVKNWNSDVRSIYSLMWLIILITLVGNLIVIVISISHFKQLHTPTNWL 61
QY 61 IHSMATVDFLLGCLVMPYSWRSABHCWYFGEVFCIKHTSTDIMLSSASIFHLSFISIDR 120
DB 62 IHSMATVDFLLGCLVMPYSWRSABHCWYFGEVFCIKHTSTDIMLSSASIFHLSFISIDR 121
QY 121 YVAVCDPLRYKAKMNLIVCMIFISWSVPAVAFGMIFLELNFKAQARLISDANOKLQIGLEMKNGI 180
DB 122 YVAVCDPLRYKAKMNLIVCMIFISWSVPAVAFGMIFLELNFKAQARLISDANOKLQIGLEMKNGI 181
QY 181 CSVFPSKISGVLTFMTSFYIPGSIIMLCVYRIYLYIAKEQARLISDANOKLQIGLEMKNGI 240
DB 182 CSVFPSKISGVLTFMTSFYIPGSIIMLCVYRIYLYIAKEQARLISDANOKLQIGLEMKNGI 241
QY 241 SOSKERKAVKTLGIWGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTFNP 300
DB 242 SOSKERKAVKTLGIWGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTFNP 301
QY 301 MYAIFYFWFRKALKMFLFGKIFQKDSRCKLFLLELSS 338
DB 302 MYAIFYFWFRKALKMFLFGKIFQKDSRCKLFLLELSS 339

RESULT 2
QBHZ64
ID QBHZ64 PRELIMINARY; PRT; 338 AA.
AC QBHZ64;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Trace amine receptor 1.
GN TARI.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OC NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Miller G.M., Madras B.K.;
RT "Cloning of Trace Amine Receptor 1 (TARI) from Rhesus Monkey.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY135366; AAN06172.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR F1.1; 1.

QY 1 MPFCHNIINISCVKNWNSDVRSIYSLMWLIILITLVGNLIVIVISISHFKQLHTPTNWL 60
DB 2 MPFCHNIINISCVKNWNSDVRSIYSLMWLIILITLVGNLIVIVISISHFKQLHTPTNWL 61
QY 61 IHSMATVDFLLGCLVMPYSWRSABHCWYFGEVFCIKHTSTDIMLSSASIFHLSFISIDR 120
DB 62 IHSMATVDFLLGCLVMPYSWRSABHCWYFGEVFCIKHTSTDIMLSSASIFHLSFISIDR 121
QY 121 YVAVCDPLRYKAKMNLIVCMIFISWSVPAVAFGMIFLELNFKAQARLISDANOKLQIGLEMKNGI 180
DB 122 YVAVCDPLRYKAKMNLIVCMIFISWSVPAVAFGMIFLELNFKAQARLISDANOKLQIGLEMKNGI 181
QY 181 CSVFPSKISGVLTFMTSFYIPGSIIMLCVYRIYLYIAKEQARLISDANOKLQIGLEMKNGI 240
DB 182 CSVFPSKISGVLTFMTSFYIPGSIIMLCVYRIYLYIAKEQARLISDANOKLQIGLEMKNGI 241
QY 241 SOSKERKAVKTLGIWGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTFNP 300
DB 242 SOSKERKAVKTLGIWGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTFNP 301
QY 301 MYAIFYFWFRKALKMFLFGKIFQKDSRCKLFLLELSS 338
DB 302 MYAIFYFWFRKALKMFLFGKIFQKDSRCKLFLLELSS 339

RESULT 3
Q923Y9
ID Q923Y9 PRELIMINARY; PRT; 332 AA.
AC Q923Y9;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Trace amine receptor 1.
GN TARI.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Sprague-Dawley;
RX MEDLINE=21374364; PubMed=11459929;
RA Borowsky B., Adham N., Jones K.A., Raddatz R., Artymyshyn R.,
RA Ogozalek K.L., Durkin M.M., Lakhani P.P., Bonini J.A., Pathirana S.,
RA Boyle N., Pu X., Kouranova E., Lichtblau H., Ochoa F.Y.,
RA Branchek T.A., Gerald C.;
RT "Trace amines: Identification of a family of mammalian G protein-
coupled receptors.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:8966-8971(2001).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AF380186; AAK71237.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR F1.1; 1.
DR PROSITE; PS00262; G-PROTEIN RECEPTOR F1.2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 332 AA; 38021 MW; ADF3A728C77B246 CRC64;

Query Match 77.9%; Score 1403; DB 11; Length 332;

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Best Local Similarity 78.1%; Pred. No. 2.5e-122; Matches 261; Conservative 27; Mismatches 44; Indels 2; Gaps 1;		
QY	1	MPFCHNIINISCVKNNNSDVRASLYSLMVLIIITLVGNLIVIVISHFQKQLHTPTNWL 60
Db	1	MHLCHNSANISHTNSNWSRDRASLYSLIILITLVGNLIVIVISHFQKQLHTPTNWL 60
QY	61	IHSMATVDLLGLCLVMPYSWVRSABHCWYFGEVFCCKHTSTDMLSASIFHLSPFISIDR 120
Db	61	IHSMATVDLLGLCLVMPYSWVRSABHCWYFGEVFCCKHTSTDMLSASIFHLSPFISIDR 120
QY	121	YAVCDPLRYKAKNNILVTCVMIFISWSVPAVFAFGMI FLELNFKGAEIYYKHVHCRCGG 180
Db	121	YAVCDPLRYKAKNNILVTCVMIFISWSVPAVFAFGMI FLELNFKGAEIYYKHVHCRCGG 180
QY	181	CVSFFSKISGVLTFMTSFYIPGSMICVYIRYLIKAEQARLISDANQKIQIGLEMKNGI 240
Db	181	CVSFFSKISGVLTFMTSFYIPGSMICVYIRYLIKAEQARLISDANQKIQIGLEMKNGI 240
QY	241	YAVCDPLRYKAKNNILVTCVMIFISWSVPAVFAFGMI FLELNFKGAEIYYKHVHCRCGG 180
Db	241	YAVCDPLRYKAKNNILVTCVMIFISWSVPAVFAFGMI FLELNFKGAEIYYKHVHCRCGG 180
QY	181	CVSFFSKISGVLTFMTSFYIPGSMICVYIRYLIKAEQARLISDANQKIQIGLEMKNGI 240
Db	181	CVSFFSKISGVLTFMTSFYIPGSMICVYIRYLIKAEQARLISDANQKIQIGLEMKNGI 240
QY	241	SOSKERKAVKTIGVNGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLWFGVYNSTENP 300
Db	241	SOSKERKAVKTIGVNGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLWFGVYNSTENP 300
QY	239	POSKETKAKTIGVNGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLWFGVYNSTENP 298
Db	239	POSKETKAKTIGVNGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLWFGVYNSTENP 298
QY	301	MYAFYFPWFRKALKMFLFGKIFQKDSRSCKLFL 334
Db	301	MYAFYFPWFRKALKMFLFGKIFQKDSRSCKLFL 334
QY	299	MYAFYFPWFRKALKMFLFGKIFQKDSRSCKLFL 332
Db	299	MYAFYFPWFRKALKMFLFGKIFQKDSRSCKLFL 332
RESULT 5		
QY	Q923Y8	PRELIMINARY; PRT; 332 AA.
Db	Q923Y8	PRELIMINARY; PRT; 332 AA.
QY	01-DEC-2001 (Tremblrel. 19, Created)	
Db	01-DEC-2001 (Tremblrel. 19, Last sequence update)	
QY	01-OCT-2003 (Tremblrel. 25, Last annotation update)	
Db	01-OCT-2003 (Tremblrel. 25, Last annotation update)	
QY	Trace amine receptor 1.	
Db	Trace amine receptor 1.	
QY	TAR1 OR TAR1	
Db	TAR1 OR TAR1	
QY	Mus musculus (Mouse)	
Db	Mus musculus (Mouse)	
QY	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Db	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
QY	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
Db	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
QY	NCBI_TaxID=10090;	
Db	NCBI_TaxID=10090;	
QY	SEQUENCE FROM N.A.	
Db	SEQUENCE FROM N.A.	
QY	STRAIN=129/SvJ;	
Db	STRAIN=129/SvJ;	
QY	MEDLINE=21374364; PubMed=11459929;	
Db	MEDLINE=21374364; PubMed=11459929;	
QY	Borowsky B., Adham N., Jones K.A., Raddatz R., Artymyshyn R.,	
Db	Borowsky B., Adham N., Jones K.A., Raddatz R., Artymyshyn R.,	
QY	Ogozalek K.L., Durkin M.M., Lakhani P.P., Bonini J.A., Pathirana S.,	
Db	Ogozalek K.L., Durkin M.M., Lakhani P.P., Bonini J.A., Pathirana S.,	
QY	Boyle N., Pu X., Kouranova E., Lichtblau H., Ochoa F.Y.,	
Db	Boyle N., Pu X., Kouranova E., Lichtblau H., Ochoa F.Y.,	
QY	Branchek T.A., Gerald C.,	
Db	Branchek T.A., Gerald C.,	
QY	Trace amines: Identification of a family of mammalian G protein-	
Db	Trace amines: Identification of a family of mammalian G protein-	
QY	coupled receptors."	
Db	coupled receptors."	
QY	Proc. Natl. Acad. Sci. U.S.A. 98:8966-8971(2001).	
Db	Proc. Natl. Acad. Sci. U.S.A. 98:8966-8971(2001).	
QY	!- SURCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).	
Db	!- SURCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).	
QY	EMBL; AF380187; AAK71238.1; --	
Db	EMBL; AF380187; AAK71238.1; --	
QY	MGD; MGI:2148258; Tarl.	
Db	MGD; MGI:2148258; Tarl.	
QY	GO:0016021; C: integral to membrane; IC.	
Db	GO:0016021; C: integral to membrane; IC.	
QY	InterPro; IPR000276; GPCR_Rhodpsn.	
Db	InterPro; IPR000276; GPCR_Rhodpsn.	
QY	Pfam; PF00001; 7tm.1; 1.	
Db	Pfam; PF00001; 7tm.1; 1.	
QY	PRINTS; PR00237; GPCR_Rhodopsin.	
Db	PRINTS; PR00237; GPCR_Rhodopsin.	
QY	PROSITE; PS00237; G PROTEIN RECEPTOR FL1; 1.	
Db	PROSITE; PS00237; G PROTEIN RECEPTOR FL1; 1.	
QY	PROSITE; PS00262; G PROTEIN RECEPTOR FL2; 1.	
Db	PROSITE; PS00262; G PROTEIN RECEPTOR FL2; 1.	
QY	G-protein coupled receptor; Receptor; Transmembrane.	
Db	G-protein coupled receptor; Receptor; Transmembrane.	
QY	SEQUENCE 332 AA; 37620 MW; 680BE692B1892264 CRC64;	
Db	SEQUENCE 332 AA; 37620 MW; 680BE692B1892264 CRC64;	
Query Match		
Best Local Similarity 75.4%; Pred. No. 1.7e-117;		
Matches 252; Conservative 31; Mismatches 49; Indels 2; Gaps 1;		
QY	1	MPFCHNIINISCVKNNNSDVRASLYSLMVLIIITLVGNLIVIVISHFQKQLHTPTNWL 60
Db	1	MHLCHAIINISHRNSDWSRVSQASLYSLMVLIIITLVGNLIVIVISHFQKQLHTPTNWL 60
QY	61	IHSMATVDLLGLCLVMPYSWVRSABHCWYFGEVFCCKHTSTDMLSASIFHLSPFISIDR 120
Db	61	IHSMATVDLLGLCLVMPYSWVRSABHCWYFGEVFCCKHTSTDMLSASIFHLSPFISIDR 120
QY	121	YAVCDPLRYKAKNNILVTCVMIFISWSVPAVFAFGMI FLELNFKGAEIYYKHVHCRCGG 180
Db	121	YAVCDPLRYKAKNNILVTCVMIFISWSVPAVFAFGMI FLELNFKGAEIYYKHVHCRCGG 180
Best Local Similarity 78.1%; Pred. No. 2.5e-122; Matches 261; Conservative 27; Mismatches 44; Indels 2; Gaps 1;		
QY	1	MPFCHNIINISCVKNNNSDVRASLYSLMVLIIITLVGNLIVIVISHFQKQLHTPTNWL 60
Db	1	MHLCHNSANISHTNSNWSRDRASLYSLIILITLVGNLIVIVISHFQKQLHTPTNWL 60
QY	61	IHSMATVDLLGLCLVMPYSWVRSABHCWYFGEVFCCKHTSTDMLSASIFHLSPFISIDR 120
Db	61	IHSMATVDLLGLCLVMPYSWVRSABHCWYFGEVFCCKHTSTDMLSASIFHLSPFISIDR 120
QY	121	YAVCDPLRYKAKNNILVTCVMIFISWSVPAVFAFGMI FLELNFKGAEIYYKHVHCRCGG 180
Db	121	YAVCDPLRYKAKNNILVTCVMIFISWSVPAVFAFGMI FLELNFKGAEIYYKHVHCRCGG 180
QY	181	CVSFFSKISGVLTFMTSFYIPGSMICVYIRYLIKAEQARLISDANQKIQIGLEMKNGI 240
Db	181	CVSFFSKISGVLTFMTSFYIPGSMICVYIRYLIKAEQARLISDANQKIQIGLEMKNGI 240
QY	241	YAVCDPLRYKAKNNILVTCVMIFISWSVPAVFAFGMI FLELNFKGAEIYYKHVHCRCGG 180
Db	241	YAVCDPLRYKAKNNILVTCVMIFISWSVPAVFAFGMI FLELNFKGAEIYYKHVHCRCGG 180
QY	181	CVSFFSKISGVLTFMTSFYIPGSMICVYIRYLIKAEQARLISDANQKIQIGLEMKNGI 240
Db	181	CVSFFSKISGVLTFMTSFYIPGSMICVYIRYLIKAEQARLISDANQKIQIGLEMKNGI 240
QY	241	SOSKERKAVKTIGVNGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLWFGVYNSTENP 300
Db	241	SOSKERKAVKTIGVNGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLWFGVYNSTENP 300
QY	239	POSKETKAKTIGVNGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLWFGVYNSTENP 298
Db	239	POSKETKAKTIGVNGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLWFGVYNSTENP 298
QY	301	MYAFYFPWFRKALKMFLFGKIFQKDSRSCKLFL 334
Db	301	MYAFYFPWFRKALKMFLFGKIFQKDSRSCKLFL 334
QY	299	MYAFYFPWFRKALKMFLFGKIFQKDSRSCKLFL 332
Db	299	MYAFYFPWFRKALKMFLFGKIFQKDSRSCKLFL 332
RESULT 4		
QY	Q8VHQ5	PRELIMINARY; PRT; 332 AA.
Db	Q8VHQ5	PRELIMINARY; PRT; 332 AA.
QY	01-MAR-2002 (Tremblrel. 20, Created)	
Db	01-MAR-2002 (Tremblrel. 20, Last sequence update)	
QY	01-JUN-2003 (Tremblrel. 24, Last annotation update)	
Db	01-JUN-2003 (Tremblrel. 24, Last annotation update)	
QY	Trace amine receptor 1.	
Db	Trace amine receptor 1.	
QY	Rattus norvegicus (Rat).	
Db	Rattus norvegicus (Rat).	
QY	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Db	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
QY	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	
Db	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	
QY	NCBI_TaxID=10116;	
Db	NCBI_TaxID=10116;	
QY	SEQUENCE FROM N.A.	
Db	SEQUENCE FROM N.A.	
QY	STRAIN=Sprague-Dawley;	
Db	STRAIN=Sprague-Dawley;	
QY	MEDLINE=21580235; PubMed=11723224;	
Db	MEDLINE=21580235; PubMed=11723224;	
QY	Bunzow J.R., Sonders M.S., Arttamangkul S., Harrison L.M., Zhang G.,	
Db	Bunzow J.R., Sonders M.S., Arttamangkul S., Harrison L.M., Zhang G.,	
QY	Quigley D.I., Darland T., Suchland K.L., Pasumamula S., Kennedy J.L.,	
Db	Quigley D.I., Darland T., Suchland K.L., Pasumamula S., Kennedy J.L.,	
QY	Olsen S.B., Megenis E., Amara S.G., Grandy D.K.,	
Db	Olsen S.B., Megenis E., Amara S.G., Grandy D.K.,	
QY	"Amphetamine, 3,4-methylenedioxymethamphetamine, lysergic acid	
Db	"Amphetamine, 3,4-methylenedioxymethamphetamine, lysergic acid	
QY	diethylamide, and metabolites of the catecholamine neurotransmitters	
Db	diethylamide, and metabolites of the catecholamine neurotransmitters	
QY	are agonists of a rat trace amine receptor."	
Db	are agonists of a rat trace amine receptor."	
QY	Mol. Pharmacol. 60:1181-1188(2001).	
Db	Mol. Pharmacol. 60:1181-1188(2001).	
QY	!- SURCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).	
Db	!- SURCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).	
QY	EMBL; AF421352; AAL65137.1; --	
Db	EMBL; AF421352; AAL65137.1; --	
QY	GO:0016021; C: integral to membrane; IEA.	
Db	GO:0016021; C: integral to membrane; IEA.	
QY	GO:0004872; F: receptor activity; IEA.	
Db	GO:0004872; F: receptor activity; IEA.	
QY	GO:0001584; F: rhodopsin-like receptor activity; IEA.	
Db	GO:0001584; F: rhodopsin-like receptor activity; IEA.	
QY	GO:0007186; P: G-protein coupled receptor protein signalin. . . ; IEA.	
Db	GO:0007186; P: G-protein coupled receptor protein signalin. . . ; IEA.	
QY	InterPro; IPR000276; GPCR_Rhodpsn.	
Db	InterPro; IPR000276; GPCR_Rhodpsn.	
QY	Pfam; PF00001; 7tm.1; 1.	
Db	Pfam; PF00001; 7tm.1; 1.	
QY	PRINTS; PR00237; GPCR_Rhodopsin.	
Db	PRINTS; PR00237; GPCR_Rhodopsin.	
QY	PROSITE; PS00237; G PROTEIN RECEPTOR FL1; 1.	
Db	PROSITE; PS00237; G PROTEIN RECEPTOR FL1; 1.	
QY	PROSITE; PS00262; G PROTEIN RECEPTOR FL2; 1.	
Db	PROSITE; PS00262; G PROTEIN RECEPTOR FL2; 1.	
QY	G-protein coupled receptor; Receptor; Transmembrane.	
Db	G-protein coupled receptor; Receptor; Transmembrane.	
QY	SEQUENCE 332 AA; 38036 MW; B6F519AFBADA0BCB6 CRC64;	
Db	SEQUENCE 332 AA; 38036 MW; B6F519AFBADA0BCB6 CRC64;	
Query Match		
Best Local Similarity 77.6%; Score 1398; DB 11; Length 332;		
Matches 261; Conservative 26; Mismatches 45; Indels 2; Gaps 1;		
QY	1	MPFCHNIINISCVKNNNSDVRASLYSLMVLIIITLVGNLIVIVISHFQKQLHTPTNWL 60
Db	1	MHLCHNSANISHTNSNWSRDRASLYSLIILITLVGNLIVIVISHFQKQLHTPTNWL 60


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Db 121 YCAVCDPLRYKAKINISTILVMILVSWSLPAVYAFQGMIFLELNKGVBEIYRSQVSDLGG 180
Qy 181 CSVFESKISGLVTEMTSPYIPQSIMLCVYRYIYLIAKEQARLIISDANKLOIGLEMKNGI 240
Db 181 CSFPFSKSVGLAFMTSPYIPQSIMLCVYRYIYLIAKEQARLIISDANKLOIGLEMKNGI 238
Qy 241 SOSKERKAVKTLIGVMGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTENP 300
Db 239 POSKETKAATLIGVMGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTENP 298
Qy 301 MYAFYFPWFRKALKMFLGKIPQKDSRSRCKLFL 334
Db 299 MYAFYFPWFRKALKMFLGKIPQKDSRSRCKLFL 332

RESULT 6
Q923Y7 PRELIMINARY; PRT; 347 AA.
AC Q923Y7;
DT 01-DEC-2001 (TremBLrel. 19, Created)
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TremBLrel. 24, Last annotation update)
DE Trace amine receptor 2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=21374364; PubMed=11459929;
RA Borowsky B., Adham N., Jones K.A., Raddatz R., Artymyshyn R.,
RA Ogozalek K.L., Durkin M.M., Lakhani P.P., Bonini J.A., Pathirana S.,
RA Boyle N., Pu X., Kouranova E., Lichtblau H., Ochoa F.Y.,
RA Branche T.A., Gerald C.;
RT "Trace amines: Identification of a family of mammalian G protein-
RT coupled receptors.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:8966-8971(2001).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AF180188; AAK71239.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR001000; Glyco_hydro_10.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00591; GLYCOSYL_HYDROL_F10; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 347 AA; 38783 MW; 86294B2876618DB9 CRC64;

Query Match 51.5%; Score 927.5; DB 11; Length 347;
Best Local Similarity 50.9%; Pred. No. 4.6e-78;
Matches 168; Conservative 64; Mismatches 97; Indels 1; Gaps 1;

Qy 3 FCNINISCVKXNNDVRSALYSMLVLIITLVGNLIVIVISHPKQLHPTNWLH 62
Db 14 FCPAANNSCPRAKAPALVVCAMYLVMIGALVMTLGNMVMVVISIAHFKQLHPTNFLIL 73
Qy 63 SMATVDFLLGCLVMPYSWRSABHCWYFGEVFCVCKHTSTDMILSSAIFHLISIDRY 122
Db 74 SMATVDFLLGCLVMPYSWRSABHCWYFGEVFCVCKHTSTDMILSSAIFHLISIDRY 133
Qy 123 AVCDDPLRYKAKMNLIVCMIFISWSVPVAFQGMIFLELNKGVBEIYRSQVSDLGG 182
Db 134 AVCDDPLRYKAKMNLIVCMIFISWSVPVAFQGMIFLELNKGVBEIYRSQVSDLGG 192
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Qy 193 VFESKISGLVTEMTSPYIPQSIMLCVYRYIYLIAKEQARLIISDANKLOIGLEMKNGISQ 242
Db 193 LIFNKLWGLASFIAPFLGALMVGIYIHFIVAKHARKIGPGRTTRALSESXWKATS 252
Qy 243 SKERKAVKTLIGVMGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTENP 302
Db 253 GKESKATKTLISVMGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTENP 312
Qy 303 YAFFYFPWFRKALKMFLGKIPQKDSRSRCKL 332
Db 313 YGMFYFPWFRKALKMFLGKIPQKDSRSRCKL 342

RESULT 7
Q9P1P5 PRELIMINARY; PRT; 306 AA.
AC Q9P1P5;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TremBLrel. 24, Last annotation update)
DE G protein-coupled receptor 58.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20149852; PubMed=10684976;
RA Lee D.K., Lynch K.R., Nguyen T., Im D.-S., Cheng R., Saldivia V.R.,
RA Liu Y., Liu I.S.C., Heng H.H.Q., Seeman P., George S.R., O'Dowd B.F.,
RA Marchese A.;
RT "Cloning and characterization of additional members of the G protein-
RT coupled receptor family.";
RL Biochim. Biophys. Acta 1490:311-323(2000).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AF112460; AAF27278.1; -.
DR Genbank; HGNC:4514; GPR58.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 306 AA; 34924 MW; 55629F613062777C CRC64;

Query Match 45.3%; Score 815; DB 4; Length 306;
Best Local Similarity 50.0%; Pred. No. 1.2e-67;
Matches 158; Conservative 48; Mismatches 86; Indels 24; Gaps 4;

Qy 25 LYSALVLIITLVGNLIVIVISHPKQLHPTNWLHSMATVDFLLGCLVMPYSWRS 84
Db 1 MYSFMAISPTITFGNLAIIISYFKQLHPTNWLHSMATVDFLLGCLVMPYSWRS 60
Qy 85 EHCWYFGEVFCVCKHTSTDMILSSAIFHLISIDRYAVCDPLRYKAKMNLIVCMIF 144
Db 61 ENCWYFGLAFCKIYYSFSLMISITIFHLCSVAIDRFALCYELLYSTKITIPVKRL 120
Qy 145 ISMSVPAVAFQGMIFLELNKGVBEIYRSQVSDLGG 204
Db 121 LCWSPGAFAGFAVGEYADGIEG-YDILVACSSCPVMFNKLWGLTFLMAQFFTPGSM 179
Qy 205 MLCVYRYIYLIAKEQARLIISDANKLOIGLEMKNGISOSKERKAVKTLIGVMGVFLIC 262
Db 180 MGVGIYKIFAVSRKHAHINLENQNNQV-----KKKKAAKTIGIVGVFLIC 229
Qy 263 WCPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTENP 322
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Db 230 WPCFTLLDPLNFSTFWLFDALTWGYNSTCNPLIYGFYFWFRALKYILLGKI 289
QY 323 F-----OKDS 327
Db 290 FSSCFHTILCMQKES 305

RESULT 8
Q9P1P4 PRELIMINARY; PRT; 343 AA.
ID Q9P1P4
AC Q9P1P4;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE G protein-coupled receptor 57.
GN GPR57.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RA Marchese A.;
RP SEQUENCE FROM N.A.
RX MEDLINE=20149852; PubMed=10684976;
RA Lee D.K., Lynch K.R., Nguyen T., Im D.-S., Cheng R., Saldivia V.R.,
RA Liu Y., Liu I.S.C., Heng H.H.Q., Seeman P., George S.R., O'Dowd B.F.,
RA Marchese A.;
RT "Cloning and characterization of additional members of the G protein-
coupled receptor family.";
RL Biochim. Biophys. Acta 1490:311-323 (2000).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
DR EMBL; AF112461; AAF27279.1; -.
DR Genbank; HGNC:4513; GPR57.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
DR G-protein coupled receptor; Receptor; Transmembrane.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 343 AA; 39065 MW; DC513D15ABBC026F CRC64;

Query Match 45.2%; Score 813.5; DB 4; Length 343;
Best Local Similarity 46.0%; Pred. No. 1.8e-67;
Matches 159; Conservative 57; Mismatches 99; Indels 31; Gaps 5;

QY 4 CHNIN-----ISCYKN-----NSNDVRASLYSLMVLIIITLVGNLIVIVSISH 49
Db 13 CPKFNKILSSHQPLFCGDNVFGYDWSHDY-----PLFGNLIVIMVSISH 58
QY 50 FKQLHTPTNWLHSMATVDFLLGCLVMPYSVRSAEHCWYFGEVCKHTSTIDMLSSAS 109
Db 59 FKQLHSPNELLNATWDFLLGFMVPSYMSRVSVCWYFGDGCKPHTSFDMLRLTS 118
QY 110 IFHLSFISIDRYAVCDPLRYAKKNILVICMIFISMSVPAVAFGMIFLELNPKGAE 169
Db 119 IFHLSIAIDRFYAVCYPLHYTTKNTSTIKQLAFCSVPALFSGFLVSEADVSGMQS 178
QY 170 IYKHVHCRGCSVPSFKISGLVLTWMTSFYIPGSLMVCVYRIYLIKEQARLISDANQ 229
Db 179 -YKILVACNFCALTFNFWGTLFTTCFFTPGSIWVGIVGKIFTVSKOHARVISHPEN 237
QY 230 LQIGLEMKNGISQSKERKAVKTLGLVMGVFLICWCPFFICTVMDPFLHYIIPPTLVN 289
Db 238 TKGA--VKHLSKKDKRAKTLGLVMGVFLACWLPCLFVLVIDPDLYSTPILIDLV 295
QY 290 WFGYLNSTFNMVYAFFYFWFRKALKMFLFGKIFOKDSSRCKLFLF 335
Db 296 WLYRFNSTCNPLIHGFFNFWQKAPKYIVSGKIFSSHSETANLPDE 341
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RESULT 9
Q923Y6 PRELIMINARY; PRT; 338 AA.
ID Q923Y6
AC Q923Y6;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Trace amine receptor 3.
GN TA3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RA Branchek T.A., Gerald C.;
RP SEQUENCE FROM N.A.
RX STRAIN=Sprague-Dawley;
RX MEDLINE=21374364; PubMed=11459929;
RA Borowsky B., Adham N., Jones K.A., Raddatz R., Artymyshyn R.,
RA Ogozalek K.L., Durkin M.M., Lakhani P.P., Bonini J.A., Pathirana S.,
RA Boyle N., Pu X., Kouranova E., Lichtblau H., Ochoa F.Y.,
RA Branchek T.A., Gerald C.;
RT "Trace amines: Identification of a family of mammalian G protein-
coupled receptors.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:8966-8971 (2001).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
DR EMBL; AF380190; AAK71241.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
DR G-protein coupled receptor; Receptor; Transmembrane.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 338 AA; 37846 MW; FBBC058A21664EA4 CRC64;

Query Match 43.4%; Score 782; DB 11; Length 338;
Best Local Similarity 45.8%; Pred. No. 1.5e-64;
Matches 154; Conservative 63; Mismatches 115; Indels 4; Gaps 4;

QY 1 MPFCNIIINISCVKNNNSNDVRASLYSLMVLIIITLVGNLIVIVSISHFKQLHTPTNWL 60
Db 1 MELCVENVNGSCIKSSYSPWPRAILYAVLGLGALLAVFGLLVITAILHFKQLHTPTNWL 60
QY 61 IHSMATVDFLLGCLVMPYSVRSAEHCWYFGEVCKHTSTIDMLSSASIFHLSFISIDR 120
Db 61 VASLACADFLVGTVMPESTVRSVEGWCYFGDTYCKPHTCFDTSFCFASLPHLCCISIDR 120
QY 121 YVAVCDPLRYAKKNILVICMIFISMSVPAVAFGMIFLELNPKGAEIYKHHVHCRGG 180
Db 121 YVAVTDPLTYTKTISVSGVCIASLWFFSVTSYFSFYTGANEIGIELVVA--UTCVGG 179
QY 181 CSVPFSKISGLVLTWMTSFYIPGSLMVCVYRIYLIKEQARLI--SDANQKLIQIGLEMKNG 239
Db 180 COAPLNQNWLLCFL--FFLPTVWVFLYGRIFLVAQKQARKIEGSANQPQASSSESYKER 238
QY 240 ISQSKERKAVKTLGLVMGVFLICWCPFFICTVMDPFLHYIIPPTLVNDFLWFGYLNSTFN 299
Db 239 VAR--RERKAATLGIAMAAFLVSWLPIYIDDAVIDAYDNFIPYAYVYIELVWCVYNSAMN 297
QY 300 PMVYAFFYFWFRKALKMFLFGKIFOKDSSRCKLFLF 335
Db 298 PLIYAFFYFWFRKALKLVSGKVFRASSSRNLFSF 333

RESULT 10
Q96RI9 PRELIMINARY; PRT; 348 AA.
ID Q96RI9
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OM protein - protein search, using sw model

Run on: October 8, 2004, 10:14:14 : Search time 57 Seconds
(without alignments)
1675.457 Million cell updates/sec

Title: US-09-633-145-2

Perfect score: 1801

Sequence: 1 MFCHNINISCKVKNWSD.....FGKIFQKDSRRCKLFLELSS 338

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq 29Jan04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1801	100.0	338	4	AAB82970 Human G p
2	1801	100.0	339	4	AAB49232 Human SNO
3	1801	100.0	339	4	AAG80973 Human nGP
4	1801	100.0	339	5	ABJ04073 Human G p
5	1801	100.0	339	5	ABG93791 Human G p
6	1801	100.0	339	5	ABP81732 Human tra
7	1786	99.2	339	5	ABP81732 Human tra
8	1539	85.5	311	7	ADCL2792 Human GPC
9	1520	84.4	296	4	AAG80972 Human nGP
10	1520	84.4	296	5	ABG93790 Human G p
11	1403	77.9	332	4	AAB49231 Rat SNORF
12	1393	77.3	332	5	ABH80695 Rat trace
13	1351	75.0	332	4	AAB49234 Mouse SNO
14	1207	67.0	238	4	AAG80960 Human nGP
15	1207	67.0	238	5	ABG93778 Human G p
16	998	55.4	191	4	AAB49230 Human SNO
17	848	47.1	351	5	ABF79888 Human SNO
18	848	47.1	351	7	ADE81115 Human SNO
19	820	45.5	319	4	AAG72332 Human OR-
20	817	45.4	306	2	AAG35831 Human G p
21	817	45.4	306	6	ABP98746 Human G p
22	815	45.3	306	6	ABP57089 Human GPC
23	815	45.3	306	6	ABP81701 Human G p
24	814.5	45.2	295	4	AAG72401 Human OR-
25	813.5	45.2	343	2	AAW59907 Human HNH

ALIGNMENTS

RESULT 1

AAB82970
ID AAB82970 standard; protein; 338 AA.

XX AAB82970;

DT 21-DEC-2001 (first entry)

DE Human G protein coupled receptor.

KW G protein coupled receptor; GPCR; aminergic receptor;

KW signal transduction; therapy; human.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Modified-site 9..12 /note= "Asn is N-glycosylated"

FT Modified-site 16..19 /note= "Asn is N-glycosylated"

FT Domain 27..47 /note= "transmembrane domain 1"

FT Domain 61..81 /note= "transmembrane domain 2"

FT Modified-site 82..89 /note= "Tyr is O-phosphorylated by tyrosine kinase"

FT Domain 99..119 /note= "transmembrane domain 3"

FT Modified-site 99..102 /note= "Thr is O-phosphorylated by casein kinase II"

FT Peptide 108..124 /note= "G protein coupled receptor signature"

FT Domain 136..156 /note= "transmembrane domain 4"

FT Modified-site 165..172 /note= "Tyr is O-phosphorylated by tyrosine kinase"

FT Domain 189..209 /note= "transmembrane domain 5"

FT Modified-site 239..244 /note= "N-myristoylated"

FT Domain 252..272 /note= "transmembrane domain 6"

FT Modified-site 253..258 /note= "N-myristoylated"

FT Modified-site 270..273 /note= "Thr is O-phosphorylated by casein kinase II"

FT Modified-site 283..286 /note= "Thr is O-phosphorylated by casein kinase II"

26	813.5	45.2	343	6	AAO19904	AAO19904 Human TA4
27	813.5	45.2	343	6	ABP81702	ABP81702 Human G p
28	782	43.4	338	3	ABJ18765	ABJ18765 Amino aci
29	743	41.3	339	6	ABJ37891	ABJ37891 NOVX prot
30	743	41.3	348	3	ABJ18764	ABJ18764 Amino aci
31	743	41.3	348	5	ABB98168	ABB98168 Human AXO
32	743	41.3	348	6	ABP81735	ABP81735 Human tra
33	743	41.3	348	7	ADE71022	ADE71022 TA3 amino
34	741.5	41.2	276	6	ABP57090	ABP57090 Mouse GPC
35	738	41.0	348	7	ADC54042	ADC54042 Human reg
36	718	39.9	345	6	ABP98101	ABP98101 Amino aci
37	715	39.7	345	4	AAG80970	AAG80970 Human nGP
38	715	39.7	345	5	AAU97600	AAU97600 Human G-p
39	715	39.7	345	5	ABJ04072	ABJ04072 Human G p
40	715	39.7	345	5	ABP52417	ABP52417 Human G p
41	715	39.7	345	5	ABG93788	ABG93788 Human G p
42	715	39.7	345	6	ABP73007	ABP73007 Amino aci
43	715	39.7	345	6	AAO19902	AAO19902 Human G-p
44	715	39.7	345	6	ABP81756	ABP81756 Human tra
45	715	39.7	628	6	AAO19907	AAO19907 Human TA4

FT Domain 287..307
 FT /note= "transmembrane domain 7"
 FT Modified-site 295..298
 FT /note= "Asn is N-glycosylated"
 FT Modified-site 327..329
 FT /note= "Ser is O-phosphorylated by protein kinase C"
 XX
 PN WO200172841-A2.
 XX
 PD 04-OCT-2001.
 XX
 XX 27-MAR-2001; 2001WO-US009660.
 XX
 XX 27-MAR-2000; 2000US-0192311P.
 PR 04-AUG-2000; 2000US-00633145.
 XX
 XX (PEKE) PE CORP NY.
 PA
 XX Kodira C, Cravchik A, Di Francesco V, Beasley EM;
 PI WPI; 2001-611617/70.
 DR N-PSDB; AAH26919, AAH26919.
 XX
 XX New human G-protein coupled receptor, useful for identifying specific
 PT modulators, potential therapeutic agents, is related to the aminergic
 PT receptor family.
 PT
 XX Claim 1; Fig 2; 60pp; English.
 PS
 CC The present sequence is that of a novel human G protein coupled receptor
 CC (GPCR) that is related to aminergic receptor family. GPCRs, particularly
 CC members of the aminergic receptor family, are a major target for drug
 CC action and development. The GPCR polypeptides and polynucleotides of the
 CC invention are therefore useful for the development of human therapeutic
 CC targets, can aid in the identification of therapeutic proteins, and serve
 CC as targets for the development of human therapeutic agents. The present
 CC GPCR is expressed in foetal brain, brain, placenta, liver, stomach and
 CC kidney, and is involved in signal transduction pathways. By targeting an
 CC agent to modulate the GPCR, the signalling activity and biological
 CC process mediated by the receptor can be agonised or antagonised in
 CC specific cells and tissues in order to modulate its biological activity
 CC in a therapeutic context (mammalian therapy) or toxic context (anti-cell
 CC therapy e.g. anti-cancer therapy)
 XX
 SQ Sequence 338 AA;
 Query Match 100.0%; Score 1801; DB 4; Length 338;
 Best Local Similarity 100.0%; Pred. No. 4.3e-199;
 Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPFCHNIINISCVKXNNSNDVRASLSYSLMVLIIITLTVGNLIVIVSISHFKQLHTPTNWL 60
 Db 1 MPFCHNIINISCVKXNNSNDVRASLSYSLMVLIIITLTVGNLIVIVSISHFKQLHTPTNWL 60
 QY 61 IHSMATVDFLLGCLVMPYSMVRSAEHCWYFGEVFCIKHTSTDIMLSSASIFHLSFISIDR 120
 Db 61 IHSMATVDFLLGCLVMPYSMVRSAEHCWYFGEVFCIKHTSTDIMLSSASIFHLSFISIDR 120
 QY 121 YVAVCDPLRYKAKMNLIVICWIFISWSVPVAFGMIFLELNFKAEEIYKHHVCRGG 180
 Db 121 YVAVCDPLRYKAKMNLIVICWIFISWSVPVAFGMIFLELNFKAEEIYKHHVCRGG 180
 QY 181 CSVFFSKISGLVTFTMTSFYIPGIMLCVYRIYLIYLAKEQARLISDANQKIQIGLEMKNGI 240
 Db 181 CSVFFSKISGLVTFTMTSFYIPGIMLCVYRIYLIYLAKEQARLISDANQKIQIGLEMKNGI 240
 QY 241 SOSKERRKAVKTLGIWVGVELICWCPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTFNP 300
 Db 241 SOSKERRKAVKTLGIWVGVELICWCPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTFNP 300
 QY 301 MYAFYFPWFRKALKMFLGKIFQKDSRRCKLFLELSS 338
 Db 301 MYAFYFPWFRKALKMFLGKIFQKDSRRCKLFLELSS 338

RESULT 2
 AAB49232
 ID AAB49232 standard; protein; 339 AA.
 XX
 AC AAB49232;
 XX
 DT 14-MAR-2001 (first entry)
 XX
 DE Human SNORF33 receptor protein.
 XX
 KW SNORF33; inflammation; arthritis; neurological disorder; infection;
 KW bone disease; respiratory disorder; asthma; cancer; cardiovascular.
 XX
 OS Homo sapiens.
 XX
 PN WO200073449-A1.
 XX
 PD 07-DEC-2000.
 XX
 PF 26-MAY-2000; 2000WO-US014654.
 XX
 PR 28-MAY-1999; 99US-00322257.
 PR 06-OCT-1999; 99US-00413433.
 XX
 XX (SYNA-) SYNAPTIC PHARM CORP.
 PA
 XX
 PI Borowsky BE, Ogozalek KL, Jones KA;
 WPI; 2001-025252/03.
 XX
 XX Nucleic acid encoding a mammalian (human, rat and mouse) SNORF33 receptor
 PT which is useful for designing drugs for treating conditions such as a
 PT chronic and acute inflammation, arthritis, neurological disorders and
 PT microbial infections.
 XX
 PS Claim 9; Fig 6; 227pp; English.
 XX
 CC The present invention relates to a mammalian SNORF33 receptor. SNORF33
 CC antagonists and agonists are used to treat abnormalities brought about by
 CC increased or decreased activity of the mammalian SNORF33 receptor. The
 CC receptor is useful as a tool for designing drugs for treating conditions
 CC such as a chronic and acute inflammation, arthritis, neurological
 CC disorders, microbial infections, bone diseases, respiratory disorders
 CC such as asthma, cancers, cardiovascular disorders
 XX
 SQ Sequence 339 AA;
 Query Match 100.0%; Score 1801; DB 4; Length 339;
 Best Local Similarity 100.0%; Pred. No. 4.3e-199;
 Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPFCHNIINISCVKXNNSNDVRASLSYSLMVLIIITLTVGNLIVIVSISHFKQLHTPTNWL 60
 Db 2 MPFCHNIINISCVKXNNSNDVRASLSYSLMVLIIITLTVGNLIVIVSISHFKQLHTPTNWL 61
 QY 61 IHSMATVDFLLGCLVMPYSMVRSAEHCWYFGEVFCIKHTSTDIMLSSASIFHLSFISIDR 120
 Db 62 IHSMATVDFLLGCLVMPYSMVRSAEHCWYFGEVFCIKHTSTDIMLSSASIFHLSFISIDR 121
 QY 121 YVAVCDPLRYKAKMNLIVICWIFISWSVPVAFGMIFLELNFKAEEIYKHHVCRGG 180
 Db 122 YVAVCDPLRYKAKMNLIVICWIFISWSVPVAFGMIFLELNFKAEEIYKHHVCRGG 181
 QY 181 CSVFFSKISGLVTFTMTSFYIPGIMLCVYRIYLIYLAKEQARLISDANQKIQIGLEMKNGI 240
 Db 182 CSVFFSKISGLVTFTMTSFYIPGIMLCVYRIYLIYLAKEQARLISDANQKIQIGLEMKNGI 241
 QY 241 SOSKERRKAVKTLGIWVGVELICWCPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTFNP 300
 Db 242 SOSKERRKAVKTLGIWVGVELICWCPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTFNP 301

QY 301 MYAFYFWRKALXKMLFGKIFQKDSRCKLFLFLSS 338
 DB 302 MYAFYFWRKALXKMLFGKIFQKDSRCKLFLFLSS 339

RESULT 3
 AAG80973
 ID AAG80973 standard; protein; 339 AA.
 XX AAG80973;
 AC AAG80973;
 XX
 DT 28-AUG-2001 (first entry)
 XX
 DE Human nGPCR56 #3.
 XX
 KW G protein-coupled receptor; nGPCR; seven transmembrane receptor;
 KW signal transduction; schizophrenia; thyroid disorder; renal failure;
 KW rheumatoid arthritis; CNS disorder; infection; metabolic disease;
 KW cardiovascular disease; proliferative disorder; hormonal disorder;
 KW neurological disorder; neuronal disorder; Alzheimer's disease; cancer;
 KW attention deficit-hyperactivity disorder/attention deficit disorder;
 KW Parkinson's disease; migraine; senile dementia; inflammatory disease;
 KW rheumatoid arthritis; autoimmune disorder; respiratory ailment;
 KW neuroprotective.
 XX
 OS Homo sapiens.
 PN WO200136473-A2.
 XX
 PD 25-MAY-2001.
 XX
 PF 16-NOV-2000; 2000WO-US031581.
 XX
 PR 16-NOV-1999; 99US-0165838P.
 PR 17-NOV-1999; 99US-0166071P.
 PR 19-NOV-1999; 99US-0166678P.
 PR 28-DEC-1999; 99US-0173396P.
 PR 28-FEB-2000; 2000US-0184129P.
 PR 28-FEB-2000; 2000US-0185421P.
 PR 28-FEB-2000; 2000US-0185554P.
 PR 02-MAR-2000; 2000US-0186530P.
 PR 03-MAR-2000; 2000US-0186811P.
 PR 09-MAR-2000; 2000US-0190310P.
 PR 17-MAR-2000; 2000US-0190310P.
 PR 21-MAR-2000; 2000US-0190800P.
 PR 20-APR-2000; 2000US-0198568P.
 PR 02-MAY-2000; 2000US-0201190P.
 PR 08-MAY-2000; 2000US-0203111P.
 PR 25-MAY-2000; 2000US-0207094P.
 XX
 PA (PHAA) PHARMACIA & UPTOWN CO.
 XX
 PI Vogeli G, Wood LS, Parodi LA, Hiebsch RR, Lind P, Slightom J;
 PI Schellin KA, Kaytes PS, Bannigan CM, Ruff V, Sejlitz T, Huff RM;
 XX
 DR WPI: 2001-389826/41.
 DR N-PSDB; AAH51013.
 XX
 PT New G protein-coupled receptor (nGPCR-x) and its encoding polynucleotide
 PT useful for diagnosing and treating e.g. schizophrenia.
 XX
 PS Claim 37; Page 92; 261pp; English.
 XX
 CC The present invention relates to novel G protein-coupled receptors
 CC (nGPCR; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27, 28,
 CC 31-38, 40, 41, 53-60) and their coding sequences. The present sequence is
 CC one such G protein-coupled receptor. GPCRs are also known as seven
 CC transmembrane receptors and function in signal transduction. The nGPCR
 CC coding sequences are useful for screening a human to diagnose a disorder
 CC affecting the brain or a genetic predisposition, specifically
 CC schizophrenia. nGPCR are useful for identifying compounds useful for
 CC treating schizophrenia. Detection of nGPCR in a sample is useful as a
 CC diagnostic tool for diseases or disorders e.g. thyroid disorders, renal

CC failure, rheumatoid arthritis, CNS disorders, infections such as HIV-1,
 CC metabolic and cardiovascular diseases, proliferative disorders and
 CC hormonal disorders. Modulators of nGPCR activity have the utility for
 CC treating neurological disorders, including schizophrenia, ADHD/ADD
 CC (attention deficit-hyperactivity disorder/attention deficit disorder),
 CC and neuronal disorders such as Alzheimer's disease, Parkinson's disease,
 CC migraine and senile dementia. Additional disorders include inflammatory
 CC conditions (e.g. Crohn's disease), rheumatoid arthritis, autoimmune
 CC diseases e.g. inflammatory bowel disease
 XX
 SQ Sequence 339 AA;
 Query Match 100.0%; Score 1801; DB 4; Length 339;
 Best Local Similarity 100.0%; Pred. No. 4.3e-199;
 Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPFCHNIINISCVKNNWSDYRASLYSLMWLIIITLVGNLIVIVSISHFKOLHTPTNWL 60
 DB 2 MPFCHNIINISCVKNNWSDYRASLYSLMWLIIITLVGNLIVIVSISHFKOLHTPTNWL 61
 QY 61 IHSMATVDFLLGCLVMPYSMVRSAEHCWYFGEVFCIKHTSTDIMLSSASIFHLSFISIDR 120
 DB 62 IHSMATVDFLLGCLVMPYSMVRSAEHCWYFGEVFCIKHTSTDIMLSSASIFHLSFISIDR 121
 QY 121 YYAVCDPLRYKAKNNILVICVMIFISWSVPVAFPMIFLELNFKGABEIIYKHHVCRGG 180
 DB 122 YYAVCDPLRYKAKNNILVICVMIFISWSVPVAFPMIFLELNFKGABEIIYKHHVCRGG 181
 QY 181 CSVFESKISGVLTFMTSFYIPGSIIMLCVYRYIYLIAKEQARLISDANOKLQIGLEMKNGI 240
 DB 182 CSVFESKISGVLTFMTSFYIPGSIIMLCVYRYIYLIAKEQARLISDANOKLQIGLEMKNGI 241
 QY 241 SQSKERKAVKTLGIVMGVFLICWCPFFICTVMDPFLHYIIPTLNDVLIWFGYLNSTNP 300
 DB 242 SQSKERKAVKTLGIVMGVFLICWCPFFICTVMDPFLHYIIPTLNDVLIWFGYLNSTNP 301
 QY 301 MYAFYFWRKALXKMLFGKIFQKDSRCKLFLFLSS 338
 DB 302 MYAFYFWRKALXKMLFGKIFQKDSRCKLFLFLSS 339

RESULT 4
 ABJ04073
 ID ABJ04073 standard; protein; 339 AA.
 XX ABJ04073;
 AC ABJ04073;
 XX
 DT 11-OCT-2002 (first entry)
 XX
 DE Human G protein coupled receptor hRUP33.
 XX
 KW Human; G-protein coupled receptor; GPCR; hRUP28; hRUP29; hRUP30; hRUP31;
 KW hRUP32; hRUP33; hRUP34; hRUP35; hRUP36; hRUP37.
 XX
 OS Homo sapiens.
 XX
 PN WO200242461-A2.
 XX
 PD 30-MAY-2002.
 XX
 PF 26-NOV-2001; 2001WO-US044386.
 XX
 PR 27-NOV-2000; 2000US-0253404P.
 PR 12-DEC-2000; 2000US-0255366P.
 PR 20-FEB-2001; 2001US-0270266P.
 PR 20-FEB-2001; 2001US-0270286P.
 PR 06-APR-2001; 2001US-0282032P.
 PR 06-APR-2001; 2001US-0282356P.
 PR 06-APR-2001; 2001US-0282358P.
 PR 14-MAY-2001; 2001US-0290917P.
 PR 31-JUL-2001; 2001US-0309208P.

XX (AREN-) ARENA PHARM INC.
 XX Chen R, Chu ZL, Dang HT, Lowitz KP, Pride C;
 XX WPI; 2002-566565/60.
 XX N-PSDB; ABT04871.
 XX Novel endogenous and non-endogenous versions of G protein-coupled
 PT receptor useful for identification of candidate compounds as receptor
 PT agonists or antagonists for use as therapeutic agents.
 XX Claim 21; Page 66-67; 84pp; English.
 XX The present invention provides the protein and coding sequences of
 CC several human G-protein coupled receptors (GPCRs). These can be used in
 CC the identification of candidate compounds as receptor agonists or inverse
 CC agonists having applicability as therapeutic agents. The present sequence
 CC is a GPCR protein of the invention
 XX Sequence 339 AA;
 SQ
 Query Match 100.0%; Score 1801; DB 5; Length 339;
 Best Local Similarity 100.0%; Pred. No. 4.3e-199;
 Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPFCHNIINISCVKNNWSDVRASLYSLMWLIILTLVGNLIVIVISISHFKQLHTPTNWL 60
 Db 2 MPFCHNIINISCVKNNWSDVRASLYSLMWLIILTLVGNLIVIVISISHFKQLHTPTNWL 61
 QY 61 IHSMATVDPLGLCLVMPYSWVRSACHWYFGVFCCKIHTSTDIMLSSASIFHLSTIDR 120
 Db 62 IHSMATVDPLGLCLVMPYSWVRSACHWYFGVFCCKIHTSTDIMLSSASIFHLSTIDR 121
 QY 121 YVAVCDPLRYKAKMNLIVCMIFISWSVPAVAFGMIFLELNFPGABEIIYKHVHCRGG 180
 Db 122 YVAVCDPLRYKAKMNLIVCMIFISWSVPAVAFGMIFLELNFPGABEIIYKHVHCRGG 181
 QY 181 CSVFSKISGVLTFMTSTYIPGIMLCVYRYLYIAKEQARLISANQKLGLEWNGI 240
 Db 182 CSVFSKISGVLTFMTSTYIPGIMLCVYRYLYIAKEQARLISANQKLGLEWNGI 241
 QY 241 SOSKERKAVKTLGIVMGVFLICWCPCFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTNP 300
 Db 242 SOSKERKAVKTLGIVMGVFLICWCPCFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTNP 301
 QY 301 MYAIFYPFWFRKALKOMLFGKIFQKDSRCKLFLELSS 338
 Db 302 MYAIFYPFWFRKALKOMLFGKIFQKDSRCKLFLELSS 339
 RESULT 5
 ID ABG93791 standard; protein; 339 AA.
 XX AC ABG93791;
 XX 26-NOV-2002 (first entry)
 XX Human G protein-coupled receptor protein, nGPCR-56, #2.
 DE
 XX Human; receptor; G protein-coupled receptor; GPCR; nGPCR; beGPCR;
 KW nGPCR protein coupled receptor; communication; serpentine structure;
 KW seven transmembrane receptor; 7TM; mental disorder; diagnosis;
 KW genetic predisposition; brain; immune response; gene therapy;
 KW anxiety disorder; depression; bipolar disorder; schizophrenia;
 KW Huntington's disease; dyskinesia; manic depression; stroke;
 KW Parkinson's disease; Alzheimer's disease; diabetes; inflammation; wound;
 KW tranquiliser.
 XX Homo sapiens.
 OS
 XX WO200264789-A1.

XX 22-AUG-2002.
 XX 14-FEB-2001; 2001WO-US004641.
 XX 14-FEB-2001; 2001WO-US004641.
 XX (PHAA) PHARMACIA & UPTJOHN CO.
 XX Lind P, Parodi LA, Vogeli G, Wood LS;
 XX WPI; 2002-674879/72.
 XX N-PSDB; ABS70246.
 XX New nucleic acids and polypeptides of the nG protein-coupled receptor,
 PT useful for treating or diagnosing a mental disorder or a disorder
 PT affecting the brain, e.g. anxiety disorders, schizophrenia, stroke or
 PT Parkinson's disease.
 XX Example 1; Page 87; 244pp; English.
 XX The invention discloses an isolated human polypeptide, and encoding
 CC nucleic acid, for a G protein-coupled receptor (GPCR), particularly the
 CC nG protein coupled receptor-14 (nGPCR-14). GPCRs are vital in the
 CC communication between cells and their environment and are characterised
 CC by a serpentine structure that passes through the cell membrane seven
 CC times, hence the reason such receptors are sometimes called seven
 CC transmembrane receptors (7TM). The polynucleotides and polypeptides are
 CC useful for identifying an nGPCR allelic variant that correlates with a
 CC mental disorder, for isolating an antibody that binds to an epitope of
 CC the polypeptide, for identifying a compound that binds the polypeptide or
 CC polynucleotide and/or modulates its biological activity, for screening a
 CC human subject to diagnose a disorder, or a genetic predisposition to a
 CC disorder, affecting the brain or a genetic disposition to the disorder,
 CC for identifying compounds useful for the treatment of a mental disorder
 CC and for identifying a compound useful as a modulator of binding between
 CC nGPCR-14 and a binding partner of nGPCR-14. The polypeptide is also
 CC useful for inducing an immune response in a mammal. The nucleic acid or
 CC polypeptide is particularly useful, using gene therapy, for treating e.g.
 CC anxiety disorders, depression, bipolar disorder, schizophrenia,
 CC Huntington's disease, dyskinesias, manic depression, stroke, Parkinson's
 CC disease or Alzheimer's disease. The nucleic acid and polypeptide may also
 CC be used for treating diabetes, inflammation or wounds. The sequences
 CC presented in ABG93791-ABG93793, ABG93795 and ABG93796 are the nGPCR (also
 CC referred to as beGPCRs) proteins
 XX Sequence 339 AA;
 SQ
 Query Match 100.0%; Score 1801; DB 5; Length 339;
 Best Local Similarity 100.0%; Pred. No. 4.3e-199;
 Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPFCHNIINISCVKNNWSDVRASLYSLMWLIILTLVGNLIVIVISISHFKQLHTPTNWL 60
 Db 2 MPFCHNIINISCVKNNWSDVRASLYSLMWLIILTLVGNLIVIVISISHFKQLHTPTNWL 61
 QY 61 IHSMATVDPLGLCLVMPYSWVRSACHWYFGVFCCKIHTSTDIMLSSASIFHLSTIDR 120
 Db 62 IHSMATVDPLGLCLVMPYSWVRSACHWYFGVFCCKIHTSTDIMLSSASIFHLSTIDR 121
 QY 121 YVAVCDPLRYKAKMNLIVCMIFISWSVPAVAFGMIFLELNFPGABEIIYKHVHCRGG 180
 Db 122 YVAVCDPLRYKAKMNLIVCMIFISWSVPAVAFGMIFLELNFPGABEIIYKHVHCRGG 181
 QY 181 CSVFSKISGVLTFMTSTYIPGIMLCVYRYLYIAKEQARLISANQKLGLEWNGI 240
 Db 182 CSVFSKISGVLTFMTSTYIPGIMLCVYRYLYIAKEQARLISANQKLGLEWNGI 241
 QY 241 SOSKERKAVKTLGIVMGVFLICWCPCFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTNP 300
 Db 242 SOSKERKAVKTLGIVMGVFLICWCPCFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTNP 301
 QY 301 MYAIFYPFWFRKALKOMLFGKIFQKDSRCKLFLELSS 338

||||| 302 MYAFAFPWFRKALXWMLFGKIFQKDSRCKLFLELSS 339

RESULT 6

ABP81732
ID ABP81732 standard; protein; 339 AA.

AC ABP81732;

DT 04-MAR-2003 (first entry)

DE Human trace amine receptor 1 protein SEQ ID NO:639.

XX G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
XX G protein-coupled receptor; modulator; antibody; immune-related disease;
XX growth-related disease; cell regeneration-related disease; AIDS; cancer;
XX immunological-related cell proliferative disease; autoimmune disease;
XX Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
XX osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
XX graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
XX psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
XX mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
XX hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
XX ulcer.

XX Homo sapiens.

OS WO200261087-A2.

PN 08-AUG-2002.

PD 19-DEC-2001; 2001WO-US050107.

PF 19-DEC-2000; 2000US-0257144P.

PR (LIFE-) LIFESPAN BIOSCIENCES INC.

PA Burner GC, Roush CL, Brown JP;

PI WPI; 2003-046718/04.

DR N-PSDB; AB242578.

XX New isolated antigenic peptides e.g., for G protein-coupled receptors
XX (GPCR), useful for diagnosing and designing drugs for treating conditions
XX in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
XX autoimmune diseases.

PS Disclosure; Fig 1; 523pp; English.

XX The present invention describes antigenic peptides (I) comprising: (a)
XX any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
XX acids. Also described: (1) an assay for the detection of a particular G
XX protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
XX and (2) an isolated antibody having high specificity and high affinity or
XX avidity for a particular GPCR. (I) can be used as GPCR modulators and in
XX gene therapy. The antigenic peptides for GPCRs are useful in detecting an
XX antibody against a particular GPCR, and in the production of specific
XX antibodies. The peptides and antibodies are also useful for detecting the
XX presence or absence of corresponding GPCRs. The antigenic peptides for
XX GPCRs and antibodies are useful for diagnosing and designing drugs for
XX treating immune-related diseases, growth-related diseases, cell
XX regeneration-related diseases, immunological-related cell proliferative
XX diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
XX atherosclerosis, bacterial, fungal, protozoan or viral infections,
XX osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
XX inflammation, allergies, Crohn's disease, diabetes, graft versus host
XX disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
XX anxiety, depression, schizophrenia, dementia, mental retardation, memory
XX loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
XX hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
XX any other disorder in which GPCRs are involved. The antibodies may be
XX used in immunoassays and immunodiagnosis. AB242523 to AB242869 encode

CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC exemplification of the present invention

XX SQ Sequence 339 AA;

Query Match 100.0%; Score 1801; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 4.3e-199;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPFCHNIINISCVKNWNSNDVRASLYSLMVLIIITLVGNLIIVIVSISHPKQLHTPTNWL 60
DB 2 MPFCHNIINISCVKNWNSNDVRASLYSLMVLIIITLVGNLIIVIVSISHPKQLHTPTNWL 61

QY 61 IHSMATVDLGLCLWMPYSWVSAEHCWYFGEVFCIKHTSTDMLSASIFHLFSISDR 120
DB 62 IHSMATVDLGLCLWMPYSWVSAEHCWYFGEVFCIKHTSTDMLSASIFHLFSISDR 121

QY 121 YVAVCDPLRYKAKNNILVICVMIFISWSVPVAFAGMIFLENFKGAETIYKGVHCRGG 180
DB 122 YVAVCDPLRYKAKNNILVICVMIFISWSVPVAFAGMIFLENFKGAETIYKGVHCRGG 181

QY 181 CSVFESKISGVLTFMTSFYIPGSIIMLCVYIRIYLIATKEQARLISDANQKLGLEMKNGI 240
DB 182 CSVFESKISGVLTFMTSFYIPGSIIMLCVYIRIYLIATKEQARLISDANQKLGLEMKNGI 241

QY 241 SOSKERKAVKTLGIWGVFLICWCPFFICTVMDPELHYIIPPTLNDVLIWFGYLNSTFNP 300
DB 242 SOSKERKAVKTLGIWGVFLICWCPFFICTVMDPELHYIIPPTLNDVLIWFGYLNSTFNP 301

QY 301 MYAFAFPWFRKALXWMLFGKIFQKDSRCKLFLELSS 338
DB 302 MYAFAFPWFRKALXWMLFGKIFQKDSRCKLFLELSS 339

RESULT 7
ABB80694

ID ABB80694 standard; protein; 339 AA.

AC ABB80694;

XX 15-JUL-2002 (first entry)

XX Human trace amine receptor.

XX Biogenic receptor; trace amine receptor; synaptic transmission; human;
XX hyperthermia; blood pressure; migraine; cardiac arrhythmia; seizure;
XX coma; diabetes; schizophrenia; hypertension; asthma; drug addiction.

XX Homo sapiens.

XX WO200222801-A2.

XX 21-MAR-2002.

XX 12-SEP-2001; 2001WO-US028455.

XX 12-SEP-2000; 2000US-00659519.

XX 09-JUL-2001; 2001US-0303967P.

XX (UYOR-) UNIV OREGON HEALTH SCI.

XX Bunzow JR, Grandy DK, Sonders M;

XX WPI; 2002-371971/40.

XX N-PSDB; ABL58316.

XX A novel mammalian biogenic amine receptor, useful in assays to identify
XX therapeutic agents for treating e.g., asthma and shock.

XX Claim 4; Fig 1; 86pp; English.

XX The invention relates to novel mammalian (human and rat) biogenic amine
XX receptors. The mammalian biogenic receptors can be used to screen for

CC compounds that bind to it, or to screen for compounds that inhibit a
 CC mammalian trace amine receptor. The compounds identified by the assay
 CC amine dependent synaptic transmission in mammals so they can be used to
 CC to treat the peripheral effects of a drug that binds to or affects the
 CC binding to trace amine receptors e.g. hyperthermia, rapid heart rate,
 CC high blood pressure, migraine, cardiac arrhythmia, seizure, coma and
 CC diabetes or to treat pathological conditions associated with elevated
 CC levels of trace amines e.g. schizophrenia, depression, hypertension,
 CC shock, cardiac arrhythmias, asthma, migraine, psychosis, anaphylactic
 CC reactions and iatrogenic conditions. They are also useful for treating
 CC drug addiction. The present sequence represents a human trace amine
 CC receptor

XX Sequence 339 AA;

SQ Query Match 99.2%; Score 1786; DB 5; Length 339;
 Best Local Similarity 99.4%; Pred. No. 2.3e-197;
 Matches 336; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MPFCHNIINISCVKNWSDVRASLSLMVLIIITLVGNLIVIVSISHFQKQLHTPTNWL 60
 DB 2 MPFCHNIINISCVKNWSDVRASLSLMVLIIITLVGNLIVIVSISHFQKQLHTPTNWL 61
 QY 61 IHSMATVDFLLGLVMPYSWVSAEHCWYFGEVFCIKHTSTDMILSSAIFHLSPISIDR 120
 DB 62 IHSMATVDFLLGLVMPYSWVSAEHCWYFGEVFCIKHTSTDMILSSAIFHLSPISIDR 121
 QY 121 YVAVCDPLRYKAKQNLIVICVMIFISWSVPAVPAFGMIFLELNFKGAEEIYKHVHCRCG 180
 DB 122 YVAVCDPLRYKAKQNLIVICVMIFISWSVPAVPAFGMIFLELNFKGAEEIYKHVHCRCG 181
 QY 181 CSVFFSKISGLVTFMTSPYIPGSLMVCVYRIYLIKAEQARLISDANQKLGLEMKNGI 240
 DB 182 CLVFFSKISGLVTFMTSPYIPGSLMVCVYRIYLIKAEQARLISDANQKLGLEMKNGI 241
 QY 241 SOSKERKAVTKTIGLVNGVFLICWCPFFICTVMDPFLHPIPTLNDVLVWFGYLNSTFNP 300
 DB 242 SOSKERKAVTKTIGLVNGVFLICWCPFFICTVMDPFLHPIPTLNDVLVWFGYLNSTFNP 301
 QY 301 MVYAFYPWFRKALKQWLFQKIFQKDSRRCKLFLELSS 338
 DB 302 MVYAFYPWFRKALKQWLFQKIFQKDSRRCKLFLELSS 339

RESULT 8
 ADC12792
 ID ADC12792 standard; protein; 311 AA.

XX ADC12792;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human GPCR protein, SEQ ID No 124.
 XX
 KW G protein-coupled receptor; GPCR; antibacterial; fungicide; protozoacide;
 KW virucide; antirheumatic; antiarthritic; tranquiliser; antidiabetic;
 KW osteopathic; neurotropic; neuroprotective; anorectic; cardiant;
 KW neuroleptic; cytostatic; antiparkinsonian; hypotensive; hypertensive;
 KW antitumor; antiallergic; anticonvulsant; analgesic; infection;
 KW rheumatoid arthritis; chronic obstructive pulmonary diseases; COPD;
 KW asthma; non-insulin dependent diabetes; obesity; osteoporosis;
 KW Alzheimer's disease; age-related macular degeneration;
 KW myocardial infarction; schizophrenia; osteoarthritis; cancer;
 KW Parkinson's disease; congestive heart failure; hypotension; hypertension;
 KW ulcer; benign prostatic hyperplasia; seizure disorder; anxiety;
 KW obsessive compulsive disorder; Cushing's syndrome; hypopituitarism; pain;
 KW human.
 XX Homo sapiens.
 XX WO2003000893-A2.
 XX

PD 03-JAN-2003.
 XX
 PP 24-JUN-2002; 2002WO-IB002357.
 XX
 PR 26-JUN-2001; 2001US-0301095P.
 PR 06-NOV-2001; 2001US-0333185P.
 XX
 PA (DECO-) DECODE GENETICS EHF.
 XX
 PI Martinez RNA, Sigurdsson GT;
 XX WPI; 2003-210155/20.
 DR N-PSDB; ADC12791.
 XX
 PT New G protein-coupled receptor (GPCR) genes and polypeptides, useful for
 PT diagnosing diseases associated with a GPCR, or in gene therapy for
 PT treating e.g. obesity, osteoporosis, Alzheimer's, cancers or congestive
 PT heart failure.
 XX
 PS Claim 10; SEQ ID NO 124; 253pp; English.
 XX
 CC The invention relates to a novel isolated nucleic acid of a G protein-
 CC coupled receptor (GPCR) gene comprising any of 62 sequences of 912-2454
 CC bp, or its complements; a GPCR polypeptide comprising any of 62 sequences
 CC of 291-818 amino acids; or a nucleic acid that hybridises, under high
 CC stringency conditions, with any of the 62 GPCR sequences or any of their
 CC complements. The GPCR agents of the invention have the following
 CC activities: antibacterial, fungicide, protozoacide, virucide,
 CC antirheumatic, tranquiliser, antiarthritic, antidiabetic, osteopathic,
 CC neurotropic, neuroprotective, anorectic, cardiant, neuroleptic, cycostatic,
 CC antiparkinsonian, hypotensive, hypertensive, antitumor, antiallergic,
 CC anticonvulsant, and analgesic. The GPCR therapeutic agent, particularly a
 CC GPCR gene agonist or antagonist, is useful for treating a disease or
 CC condition associated with a GPCR in an individual. The nucleic acid cited
 CC above, which is 100 or fewer nucleotides in length, is useful for
 CC assaying a sample for the presence of the GPCR gene nucleic acid or a
 CC GPCR gene nucleic acid with at least one nucleotide difference from a
 CC first nucleic acid, or for diagnosing a susceptibility to a disease or
 CC conditions associated with a GPCR. These diseases include infections
 CC (e.g. bacterial, fungal, protozoan or viral), rheumatoid arthritis,
 CC chronic obstructive pulmonary diseases (COPD), asthma, non-insulin
 CC dependent diabetes, obesity, osteoporosis, Alzheimer's disease, age-
 CC related macular degeneration, myocardial infarction, schizophrenia,
 CC osteoarthritis, cancers, Parkinson's diseases, congestive heart failure,
 CC hypotension, hypertension, ulcers, allergies, benign prostatic
 CC hyperplasia, seizure disorder, anxiety, obsessive compulsive disorder,
 CC Cushing's syndrome, hypopituitarism, or pain. This sequence represents
 CC one of the 62 GPCR proteins of the invention.
 XX
 SQ Sequence 311 AA;

Query Match 85.5%; Score 1539; DB 7; Length 311;
 Best Local Similarity 100.0%; Pred. No. 7.5e-169;
 Matches 289; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 28 LMVLIITLVGNLIVIVSISHFQKQLHTPTNWLHSMATVDFLLGLVMPYSWVSAEHC 87
 DB 23 LMVLIITLVGNLIVIVSISHFQKQLHTPTNWLHSMATVDFLLGLVMPYSWVSAEHC 82
 QY 88 WYFGEVFCIKHTSTDMILSSAIFHLSPISIDRYAVCDPLRYKAKQNLIVICWIFISW 147
 DB 83 WYFGEVFCIKHTSTDMILSSAIFHLSPISIDRYAVCDPLRYKAKQNLIVICWIFISW 142
 QY 148 SVPAVFAFGMIFLELNFKGAEEIYKHVHCRCGSCSVFFSKISGLVTFMTSPYIPGSLMCL 207
 DB 143 SVPAVFAFGMIFLELNFKGAEEIYKHVHCRCGSCSVFFSKISGLVTFMTSPYIPGSLMCL 202
 QY 208 VYVRIYLIKAEQARLISDANQKLGLEMKNGISQSKERKAVTKLGVWGVFLICWCPFF 267
 DB 203 VYVRIYLIKAEQARLISDANQKLGLEMKNGISQSKERKAVTKLGVWGVFLICWCPFF 262
 QY 268 ICTVMDPFLHPIPTLNDVLVWFGYLNSTFNPVYAFYFWRKALKM 316

DB 263 ICTVMDPFLHYIIPPTLNDVLWFGYNGSTENDMVYAFYFPERKALKM 311

RESULT 9

AA80972

ID AAG80972 standard; protein; 296 AA.

AC AAG80972;

XX

DT 28-AUG-2001 (first entry)

XX

DE Human nGPCR56 #2.

XX

XX G protein-coupled receptor; nGPCR; seven transmembrane receptor;

KW signal transduction; schizophrenia; thyroid disorder; renal failure;

KW rheumatoid arthritis; CNS disorder; infection; metabolic disease;

KW cardiovascular disease; proliferative disorder; hormonal disorder;

KW neurological disorder; neuronal disorder; Alzheimer's disease; cancer;

KW attention deficit-hyperactivity disorder/attention deficit disorder;

KW Parkinson's disease; migraine; senile dementia; inflammatory disease;

KW rheumatoid arthritis; autoimmune disorder; respiratory ailment;

XX neuroprotective.

OS Homo sapiens.

XX

PN WO200136473-A2.

XX

PD 25-MAY-2001.

XX

PF 16-NOV-2000; 2000WO-US031581.

XX

PR 16-NOV-1999; 99US-0165838P.

PR 17-NOV-1999; 99US-0166071P.

PR 19-NOV-1999; 99US-0166678P.

PR 28-DEC-1999; 99US-0173396P.

PR 22-FEB-2000; 2000US-0184129P.

PR 28-FEB-2000; 2000US-0185421P.

PR 28-FEB-2000; 2000US-0185554P.

PR 02-MAR-2000; 2000US-0186530P.

PR 03-MAR-2000; 2000US-0186811P.

PR 09-MAR-2000; 2000US-0188114P.

PR 17-MAR-2000; 2000US-0190310P.

PR 21-MAR-2000; 2000US-0190800P.

PR 20-APR-2000; 2000US-0198568P.

PR 02-MAY-2000; 2000US-0201190P.

PR 08-MAY-2000; 2000US-0203111P.

PR 25-MAY-2000; 2000US-0207094P.

XX

PA (PHAA) PHARMACIA & UPJOHN CO.

XX

PI Vogeli G, Wood LS, Parodi LA, Hiebach RR, Lind P, Slightom J;

PI Schellin KA, Kaytes PS, Bannigan CM, Ruff V, Sejlitz T, Huff RM;

XX

DR WPI; 2001-389826/41.

DR N-PSDB; AAH51012.

XX

XX New G protein-coupled receptor (nGPCR-x) and its encoding polynucleotide

PT useful for diagnosing and treating e.g. schizophrenia.

XX

PS Claim 37; Page 91-92; 261pp; English.

XX

CC The present invention relates to novel G protein-coupled receptors

CC (nGPCR; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27, 28,

CC 31-38, 40, 41, 53-60) and their coding sequences. The present sequence is

CC one such G protein-coupled receptor. GPCRs are also known as seven

CC transmembrane receptors and function in signal transduction. The nGPCR

CC coding sequences are useful for screening a human to diagnose a disorder

CC affecting the brain or a genetic predisposition, specifically

CC schizophrenia. nGPCR are useful for identifying compounds useful for

CC treating schizophrenia. Detection of nGPCR in a sample is useful as a

CC diagnostic tool for diseases or disorders e.g. thyroid disorders, renal

CC failure, rheumatoid arthritis, CNS disorders, infections such as HIV-1,

CC metabolic and cardiovascular diseases, proliferative disorders and

CC

CC hormonal disorders. Modulators of nGPCR activity have the utility for

CC treating neurological disorders, including schizophrenia, ADHD/ADD

CC (attention deficit-hyperactivity disorder/attention deficit disorder),

CC and neuronal disorders such as Alzheimer's disease, Parkinson's disease,

CC migraine and senile dementia. Additional disorders include inflammatory

CC conditions (e.g. Crohn's disease), rheumatoid arthritis, autoimmune

CC disorders, cancers, respiratory ailments such as asthma, and inflammatory

XX diseases e.g. inflammatory bowel disease

XX

SQ Sequence 296 AA;

Query Match 84.4%; Score 1520; DB 4; Length 296;

Best Local Similarity 100.0%; Pred. No. 1,1e-166; Indels 0; Gaps 0;

Matches 286; Conservative 0; Mismatches 0;

QY 1 MPFCHNIINISCVKNNSNDVRASLYSLMVLIIITLVGNLIVIVISHFQKQLHTPTNWL 60

DB |||||

2 MPFCHNIINISCVKNNSNDVRASLYSLMVLIIITLVGNLIVIVISHFQKQLHTPTNWL 61

QY 61 IHSMATVDLGLCLVMPYSMVRSAEHCWYFGEVFCIKHTSTOIMLSSAIFHLSPFISDR 120

DB |||||

62 IHSMATVDLGLCLVMPYSMVRSAEHCWYFGEVFCIKHTSTOIMLSSAIFHLSPFISDR 121

QY 121 YVAVCDPLRYKAKMNLIVICVMIFISWSVPVAFGMIFELNFKGAEEIYKHHVHCRGG 180

DB |||||

122 YVAVCDPLRYKAKMNLIVICVMIFISWSVPVAFGMIFELNFKGAEEIYKHHVHCRGG 181

QY 181 CSVFFSKISGVLTFMTSFYIPGSIMLCVYRIYLIKAQARLISDANQKLIQIGLEMKNGI 240

DB |||||

182 CSVFFSKISGVLTFMTSFYIPGSIMLCVYRIYLIKAQARLISDANQKLIQIGLEMKNGI 241

QY 241 SOSKERKAVKTLGIVNGVELICWCPFFICTVMDPFLHYIIPPTLND 286

DB |||||

242 SOSKERKAVKTLGIVNGVELICWCPFFICTVMDPFLHYIIPPTLND 287

RESULT 10

ABG93790

ID ABG93790 standard; protein; 296 AA.

AC ABG93790;

XX

DT 26-NOV-2002 (first entry)

XX

DE Human G protein-coupled receptor protein, nGPCR-56, #1.

XX

KW Human; receptor; G protein-coupled receptor; GPCR; nGPCR; beGPCR;

KW nG protein coupled receptor; communication; serpentine structure;

KW seven transmembrane receptor; 7TM; mental disorder; diagnosis;

KW genetic predisposition; brain; immune response; gene therapy;

KW anxiety disorder; depression; bipolar disorder; schizophrenia;

KW Huntington's disease; dyskinesia; manic depression; stroke;

KW Parkinson's disease; Alzheimer's disease; diabetes; inflammation; wound;

KW tranquilliser.

OS Homo sapiens.

XX

XX WO200264789-A1.

PN

XX 22-AUG-2002.

XX

PF 14-FEB-2001; 2001WO-US004641.

XX

PR 14-FEB-2001; 2001WO-US004641.

XX

PA (PHAA) PHARMACIA & UPJOHN CO.

XX

PI Lind P, Parodi LA, Vogeli G, Wood LS;

XX

DR WPI; 2002-674879/72.

DR N-PSDB; ABS70245.

XX

PT New nucleic acids and polypeptides of the nG protein-coupled receptor,

PT useful for treating or diagnosing a mental disorder or a disorder
PT affecting the brain, e.g. anxiety disorders, schizophrenia, stroke or
XX Parkinson's disease.
XX
XX Example 1; Page 86-87; 244pp; English.
XX
XX The invention discloses an isolated human polypeptide, and encoding
CC nucleic acid, for a G protein-coupled receptor (GPCR), particularly the
CC ng protein coupled receptor-14 (ngPCR-14). GPCRs are vital in the
CC communication between cells and their environment and are characterised
CC by a serpentine structure that passes through the cell membrane seven
CC times, hence the reason such receptors are sometimes called seven
CC transmembrane receptors (7TM). The polynucleotides and polypeptides are
CC useful for identifying an nPCR allelic variant that correlates with a
CC mental disorder, for isolating an antibody that binds to an epitope of
CC the polypeptide, for identifying a compound that binds the polypeptide or
CC polynucleotide and/or modulates its biological activity, for screening a
CC human subject to diagnose a disorder, or a genetic predisposition to a
CC disorder, affecting the brain or a genetic disposition to the disorder,
CC for identifying compounds useful for the treatment of a mental disorder,
CC and for identifying a compound useful as a modulator of binding between
CC ngPCR-14 and a binding partner of ngPCR-14. The polypeptide is also
CC useful for inducing an immune response in a mammal. The nucleic acid or
CC polypeptide is particularly useful, using gene therapy, for treating e.g.
CC anxiety disorders, depression, bipolar disorder, schizophrenia,
CC Huntington's disease, dyskinesias, manic depression, stroke, Parkinson's
CC disease or Alzheimer's disease. The nucleic acid and polypeptide may also
CC be used for treating diabetes, inflammation or wounds. The sequences
CC presented in ABG93747-ABG93793, ABG93795 and ABG93796 are the nPCR (also
CC referred to as beGPCR) proteins
XX
XX Sequence 296 AA;

Query Match 84.4%; Score 1520; DB 5; Length 296;
Best Local Similarity 100.0%; Pred. No. 1.1e-166;
Matches 286; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPFCNNINISCVKNWNSDVRASLYSLMVLIIITLVGNLIVIVISHSFKQLHTPTNWL 60
Db 2 MPFCNNINISCVKNWNSDVRASLYSLMVLIIITLVGNLIVIVISHSFKQLHTPTNWL 61
QY 61 IHSMATVDFLLGCLVMPYSNVRSAEHCWYFGEVFCIKHTSTDMILSSASIFHLSFIDSIDR 120
Db 62 IHSMATVDFLLGCLVMPYSNVRSAEHCWYFGEVFCIKHTSTDMILSSASIFHLSFIDSIDR 121
QY 121 YVAVCDPLRYKAKWNTLVICVMIFISWSVPAPVAFGMIFELNFKGAEEIYKHHVCRGG 180
Db 122 YVAVCDPLRYKAKWNTLVICVMIFISWSVPAPVAFGMIFELNFKGAEEIYKHHVCRGG 181
QY 181 CSVFFSKISGVLTFMTSFYIPGSIIMLCVYRIYLIKAEQARLISDANQKLIQGLEMKNGI 240
Db 182 CSVFFSKISGVLTFMTSFYIPGSIIMLCVYRIYLIKAEQARLISDANQKLIQGLEMKNGI 241
QY 241 SQSKERKAVKTLGIWGVFLICWCPFFICTVMDPFLHYIIPPTLND 286
Db 242 SQSKERKAVKTLGIWGVFLICWCPFFICTVMDPFLHYIIPPTLND 287

RESULT 11
AAB49231
ID AAB49231 standard; protein; 332 AA.
XX
XX AAB49231;
XX
XX 14-MAR-2001 (first entry)
XX
XX Rat SNORF33 receptor protein.
XX
XX SNORF33; inflammation; arthritis; neurological disorder; infection;
XX bone disease; respiratory disorder; asthma; cancer; cardiovascular.
XX
XX Rattus rattus.
XX

PN WO200073449-A1.
XX
XX 07-DEC-2000.
XX
XX 26-MAY-2000; 2000WO-US014654.
XX
XX 28-MAY-1999; 99US-00322257.
XX 06-OCT-1999; 99US-00413433.
XX (SYNA-) SYNAPTIC PHARM CORP.
XX
XX Borowsky BE, Ogozalek KL, Jones KA;
XX WPI; 2001-025252/03.
XX
XX Nucleic acid encoding a mammalian (human, rat and mouse) SNORF33 receptor
XX which is useful for designing drugs for treating conditions such as a
XX chronic and acute inflammation, arthritis, neurological disorders and
XX microbial infections.
XX
XX Claim 12; Fig 4; 227pp; English.
XX
XX The present invention relates to a mammalian SNORF33 receptor. SNORF33
XX antagonists and agonists are used to treat abnormalities brought about by
XX increased or decreased activity of the mammalian SNORF33 receptor. The
XX receptor is useful as a tool for designing drugs for treating conditions
XX such as a chronic and acute inflammation, arthritis, neurological
XX disorders, microbial infections, bone diseases, respiratory disorders
XX such as asthma, cancers, cardiovascular disorders
XX
XX Sequence 332 AA;
Query Match 77.9%; Score 1403; DB 4; Length 332;
Best Local Similarity 78.1%; Pred. No. 4.4e-153;
Matches 261; Conservative 27; Mismatches 44; Indels 2; Gaps 1;
QY 1 MPFCNNINISCVKNWNSDVRASLYSLMVLIIITLVGNLIVIVISHSFKQLHTPTNWL 60
Db 1 MHLCHNSANISHTNSNWSRDSVSLSLIITLVGNLIVIVISHSFKQLHTPTNWL 60
QY 61 IHSMATVDFLLGCLVMPYSNVRSAEHCWYFGEVFCIKHTSTDMILSSASIFHLSFIDSIDR 120
Db 61 LHSMATVDFLLGCLVMPYSNVRSAEHCWYFGEVFCIKHTSTDMILSSASIFHLSFIDSIDR 120
QY 121 YVAVCDPLRYKAKWNTLVICVMIFISWSVPAPVAFGMIFELNFKGAEEIYKHHVCRGG 180
Db 121 YVAVCDPLRYKAKWNTLVICVMIFISWSVPAPVAFGMIFELNFKGAEEIYKHHVCRGG 180
QY 181 CSVFFSKISGVLTFMTSFYIPGSIIMLCVYRIYLIKAEQARLISDANQKLIQGLEMKNGI 240
Db 181 CFPFFSKISGVLTFMTSFYIPGSIIMLCVYRIYLIKAEQARLISDANQKLIQGLEMKNGI 240
QY 241 SQSKERKAVKTLGIWGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTFNP 300
Db 239 PQSKETKAAKTLGIWGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTFNP 298
QY 301 MYVAFYPMFRKALXMMLEFKIFQKDSRSKCLPL 334
Db 299 MYVAFYPMFRKALXMMLEFKIFQKDSRSKCLPL 332
XX
XX RESULT 12
XX ABB80695
XX ID ABB80695 standard; protein; 332 AA.
XX
XX ABB80695;
XX
XX 15-JUL-2002 (first entry)
XX
XX Rat trace amine receptor.
XX
XX Biogenic receptor; trace amine receptor; synaptic transmission; rat;
XX hyperthermia; blood pressure; migraine; cardiac arrhythmia; seizure;
XX

```

KW coma; diabetes; schizophrenia; hypertension; asthma; drug addiction.
XX Rattus norvegicus.
OS WO200222801-A2.
PN 21-MAR-2002.
XX 12-SEP-2001; 2001WO-US028455.
XX 12-SEP-2000; 2000US-00659519.
PR 09-JUL-2001; 2001US-0303967P.
XX (UYOR-) UNIV OREGON HEALTH SCI.
PA Bunzow JR, Grandy DK, Sonders M;
XX WPI; 2002-371971/40.
XX N-PSDB; ABL58317.
DR A novel mammalian biogenic amine receptor, useful in assays to identify
XX therapeutic agents for treating e.g., asthma and shock.
XX Claim 5; Fig 2; 86pp; English.
XX The invention relates to novel mammalian (human and rat) biogenic amine
XX receptors. The mammalian biogenic receptors can be used to screen for
XX compounds that bind to it, or to screen for compounds that inhibit a
XX mammalian trace amine receptor. The compounds identified by the assay
XX methods can be used to reduce sympathomimetic effects of enhanced trace
XX amine dependent synaptic transmission in mammals so they can be used to
XX treat the peripheral effects of a drug that binds to or affects the
XX binding to trace amine receptors e.g. hyperthermia, rapid heart rate,
XX high blood pressure, migraine, cardiac arrhythmia, seizure, coma and
XX diabetes or to treat pathological conditions associated with elevated
XX levels of trace amines e.g. schizophrenia, depression, hypertension,
XX shock, cardiac arrhythmias, asthma, migraine, psychosis, anaphylactic
XX reactions and iatrogenic conditions. They are also useful for treating
XX drug addiction. The present sequence represents a rat trace amine
XX receptor
XX
XX Sequence 332 AA;
XX
XX Query Match 77.3%; Score 1393; DB 5; Length 332;
XX Best Local Similarity 77.5%; Pred. No. 6.2e-152;
XX Matches 259; Conservative 27; Mismatches 46; Indels 2; Gaps 1;
QY 1 MPFCHNIINISCVKXNNSNDVRASLYSLMVLIIITLVGNLIVIVISISHFKQLHTPTNWL 60
DB 1 MELCHNSANISHTNRNRSRDRASLYSLMVLIIITLVGNLIVIVISISHFKQLHTPTNWL 60
QY 61 IHSMATVDFLLGCLVMPYSWVRSACHWYFGEVFCCKIHTSTDIMLSSASIFHLSPFISIDR 120
DB 61 LHSMAVDFLLGCLVMPYSWVRSACHWYFGEVFCCKIHTSTDIMLSSASIFHLSPFISIDR 120
QY 121 YVAVCDPLRYKAKMILVTCVMIFISWSVPVAFAGMIFLELNFKGAEIYKHHVCRGG 180
DB 121 YVAVCDPLRYKAKINIAALFWMLISWSLPVAVAFAGMIFLELNFKGAEIYKHHVCRGG 180
QY 181 CSVFFSKISGLVTFMTSFYIPGSIIMLCVYRIYLIJAKEQARLISDANKQLQIGLEMKNGI 240
DB 181 CFLFFSKVSGVLAFTSFYIPGSIIMLCVYRIYLIJAKEQARLISDANKQLQIGLEMKNGI 240
QY 241 SOSKERKAVKTIGVWGVLICWCPFFICTWMDPFLHYIIPPTLNDVLWFGYLNSTNP 300
DB 239 POSKETKAAKTIGVWGVLICWCPFFICTWMDPFLHYIIPPTLNDVLWFGYLNSTNP 298
QY 301 MYAFYFPWFRKALKMWLFGKIFQKDSRSCKLFL 334
DB 299 MYAFYFPWFRKALKMWLFGKIFQKDSRSCKLFL 332
XX
XX RESULT 13

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comat; diabetes; schizophrenia; hypertension; asthma; drug addiction.

Rattus norvegicus.

WO200222801-A2.

21-MAR-2002.

12-SEP-2001; 2001WO-US028455.

12-SEP-2000; 2000US-00659519.

09-JUL-2001; 2001US-0303967P.

(UYOR-) UNIV OREGON HEALTH SCI.

Bunzow JR, Grandy DK, Sonders M;

WPI; 2002-371971/40.

N-PSDB; ABL58317.

A novel mammalian biogenic amine receptor, useful in assays to identify therapeutic agents for treating e.g., asthma and shock.

Claim 5; Fig 2; 86pp; English.

The invention relates to novel mammalian (human and rat) biogenic amine receptors. The mammalian biogenic receptors can be used to screen for compounds that bind to it, or to screen for compounds that inhibit a mammalian trace amine receptor. The compounds identified by the assay methods can be used to reduce sympathomimetic effects of enhanced trace amine dependent synaptic transmission in mammals so they can be used to treat the peripheral effects of a drug that binds to or affects the binding to trace amine receptors e.g. hyperthermia, rapid heart rate, high blood pressure, migraine, cardiac arrhythmia, seizure, coma and diabetes or to treat pathological conditions associated with elevated levels of trace amines e.g. schizophrenia, depression, hypertension, shock, cardiac arrhythmias, asthma, migraine, psychosis, anaphylactic reactions and iatrogenic conditions. They are also useful for treating drug addiction. The present sequence represents a rat trace amine receptor

Sequence 332 AA;

Query Match 77.3%; Score 1393; DB 5; Length 332;

Best Local Similarity 77.5%; Pred. No. 6.2e-152;

Matches 259; Conservative 27; Mismatches 46; Indels 2; Gaps 1;

QY 1 MPFCHNIINISCVKXNNSNDVRASLYSLMVLIIITLVGNLIVIVISISHFKQLHTPTNWL 60

DB 1 MELCHNSANISHTNRNRSRDRASLYSLMVLIIITLVGNLIVIVISISHFKQLHTPTNWL 60

QY 61 IHSMATVDFLLGCLVMPYSWVRSACHWYFGEVFCCKIHTSTDIMLSSASIFHLSPFISIDR 120

DB 61 LHSMAVDFLLGCLVMPYSWVRSACHWYFGEVFCCKIHTSTDIMLSSASIFHLSPFISIDR 120

QY 121 YVAVCDPLRYKAKMILVTCVMIFISWSVPVAFAGMIFLELNFKGAEIYKHHVCRGG 180

DB 121 YVAVCDPLRYKAKINIAALFWMLISWSLPVAVAFAGMIFLELNFKGAEIYKHHVCRGG 180

QY 181 CSVFFSKISGLVTFMTSFYIPGSIIMLCVYRIYLIJAKEQARLISDANKQLQIGLEMKNGI 240

DB 181 CFLFFSKVSGVLAFTSFYIPGSIIMLCVYRIYLIJAKEQARLISDANKQLQIGLEMKNGI 240

QY 241 SOSKERKAVKTIGVWGVLICWCPFFICTWMDPFLHYIIPPTLNDVLWFGYLNSTNP 300

DB 239 POSKETKAAKTIGVWGVLICWCPFFICTWMDPFLHYIIPPTLNDVLWFGYLNSTNP 298

QY 301 MYAFYFPWFRKALKMWLFGKIFQKDSRSCKLFL 334

DB 299 MYAFYFPWFRKALKMWLFGKIFQKDSRSCKLFL 332

RESULT 13

AA849234

ID AAB49234 standard; protein; 332 AA.

XX AAB49234;

XX 14-MAR-2001 (first entry)

DE Mouse SNORF33 receptor protein.

XX SNORF33; inflammation; arthritis; neurological disorder; infection;

KW bone disease; respiratory disorder; asthma; cancer; cardiovascular.

OS Mus musculus.

XX WO200073449-A1.

PN 07-DEC-2000.

XX 26-MAY-2000; 2000WO-US014654.

XX 28-MAY-1999; 99US-00322257.

PR 06-OCT-1999; 99US-00413433.

XX (SYNA-) SYNAPTIC PHARM CORP.

PA Borowsky BE, Ogozalek KL, Jones KA;

XX WPI; 2001-025252/03.

DR Nucleic acid encoding a mammalian (human, rat and mouse) SNORF33 receptor

XX which is useful for designing drugs for treating conditions such as a

PT chronic and acute inflammation, arthritis, neurological disorders and

PT microbial infections.

XX Claim 15; Fig 20; 227pp; English.

XX The present invention relates to a mammalian SNORF33 receptor. SNORF33

CC antagonists and agonists are used to treat abnormalities brought about by

CC increased or decreased activity of the mammalian SNORF33 receptor. The

CC receptor is useful as a tool for designing drugs for treating conditions

CC such as a chronic and acute inflammation, arthritis, neurological

CC disorders, microbial infections, bone diseases, respiratory disorders

CC such as asthma, cancers, cardiovascular disorders

XX Sequence 332 AA;

XX Query Match 75.0%; Score 1351; DB 4; Length 332;

XX Best Local Similarity 75.4%; Pred. No. 4.5e-147;

XX Matches 252; Conservative 31; Mismatches 49; Indels 2; Gaps 1;

QY 1 MPFCHNIINISCVKXNNSNDVRASLYSLMVLIIITLVGNLIVIVISISHFKQLHTPTNWL 60
DB 1 MELCHAITNISHRNSDWSREVQASLYSLMVLIIITLVGNLIVIVISISHFKQLHTPTNWL 60
QY 61 IHSMATVDFLLGCLVMPYSWVRSACHWYFGEVFCCKIHTSTDIMLSSASIFHLSPFISIDR 120
DB 61 LHSMAVDFLLGCLVMPYSWVRSACHWYFGEVFCCKIHTSTDIMLSSASIFHLSPFISIDR 120
QY 121 YVAVCDPLRYKAKMILVTCVMIFISWSVPVAFAGMIFLELNFKGAEIYKHHVCRGG 180
DB 121 YVAVCDPLRYKAKINISITLWMLISWSLPVAVAFAGMIFLELNFKGAEIYKHHVCRGG 180
QY 181 CSVFFSKISGLVTFMTSFYIPGSIIMLCVYRIYLIJAKEQARLISDANKQLQIGLEMKNGI 240
DB 181 CSPFFSKVSGVLAFTSFYIPGSIIMLCVYRIYLIJAKEQARLISDANKQLQIGLEMKNGI 240
QY 241 SOSKERKAVKTIGVWGVLICWCPFFICTWMDPFLHYIIPPTLNDVLWFGYLNSTNP 300
DB 239 POSKETKAAKTIGVWGVLICWCPFFICTWMDPFLHYIIPPTLNDVLWFGYLNSTNP 298
QY 301 MYAFYFPWFRKALKMWLFGKIFQKDSRSCKLFL 334
DB 299 MYAFYFPWFRKALKMWLFGKIFQKDSRSCKLFL 332

RESULT 14

AAG80960

ID AAG80960 standard; protein; 238 AA.

AC AAG80960;

XX 28-AUG-2001 (first entry)

XX Human nGPCR56 #1.

KW G protein-coupled receptor; nGPCR; seven transmembrane receptor;
KW signal transduction; schizophrenia; thyroid disorder; renal failure;
KW rheumatoid arthritis; CNS disorder; infection; metabolic disease;
KW cardiovascular disease; proliferative disorder; hormonal disorder;
KW neurological disorder; neuronal disorder; Alzheimer's disease; cancer;
KW attention deficit-hyperactivity disorder/attention deficit disorder;
KW Parkinson's disease; migraine; senile dementia; inflammatory disease;
KW rheumatoid arthritis; autoimmune disorder; respiratory ailment;
KW neuroprotective.

XX Homo sapiens.

XX WO200136473-A2.

XX 25-MAY-2001.

XX 16-NOV-2000; 2000WO-US031581.

XX 16-NOV-1999; 99US-0165838P.

XX 17-NOV-1999; 99US-0166071P.

XX 19-NOV-1999; 99US-0166678P.

XX 28-DEC-1999; 99US-0173396P.

XX 22-FEB-2000; 2000US-0184129P.

XX 28-FEB-2000; 2000US-0185421P.

XX 28-FEB-2000; 2000US-0185554P.

XX 02-MAR-2000; 2000US-0186530P.

XX 03-MAR-2000; 2000US-0186811P.

XX 09-MAR-2000; 2000US-0188114P.

XX 17-MAR-2000; 2000US-0190310P.

XX 21-MAR-2000; 2000US-0190800P.

XX 20-APR-2000; 2000US-0198568P.

XX 02-MAY-2000; 2000US-0201190P.

XX 08-MAY-2000; 2000US-0203111P.

XX 25-MAY-2000; 2000US-0207094P.

XX (PHAA) PHARMACIA & UPJOHN CO.

XX Vogeli G, Wood LS, Parodi LA, Hiebach RR, Lind P, Slightom J;

XX Schellin KA, Kaytes PS, Bannigan CM, Ruff V, Sejlitz T, Huff RM;

XX WPI; 2001-389826/41.

XX N-PSDB; AAH51000.

XX New G protein-coupled receptor (nGPCR-x) and its encoding polynucleotide

XX useful for diagnosing and treating e.g. schizophrenia.

XX Claim 37; Page 86; 261pp; English.

CC treating neurological disorders, including schizophrenia, ADHD/ADD
CC (attention deficit-hyperactivity disorder/attention deficit disorder),
CC and neuronal disorders such as Alzheimer's disease, Parkinson's disease,
CC migraine and senile dementia. Additional disorders include inflammatory
CC conditions (e.g. Crohn's disease), rheumatoid arthritis, autoimmune
CC disorders, cancers, respiratory ailments such as asthma, and inflammatory
CC diseases e.g. inflammatory bowel disease

XX SQ Sequence 238 AA;

Query Match 67.0%; Score 1207; DB 4; Length 238;

Best Local Similarity 100.0%; Pred. No. 1.3e-130;

Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPFCNNINISCVKNNWSDVRASLYSLMVLIIITLVGNLIVIVISHFQKLTPTNWL 60

Db 11 MPFCNNIINISCVKNNWSDVRASLYSLMVLIIITLVGNLIVIVISHFQKLTPTNWL 70

QY 61 IHSMATVDFLLGCLVMPYSMVRSAEHCWYFGEVFCIKHTSTDIMLSSASIFHLSFISIDR 120

Db 71 IHSMATVDFLLGCLVMPYSMVRSAEHCWYFGEVFCIKHTSTDIMLSSASIFHLSFISIDR 130

QY 121 YYAVCDPLRYKAKNNILVICVMIFISWSVPVAFGMIFELNFKGAEEIYYKHVHCRGG 180

Db 131 YYAVCDPLRYKAKNNILVICVMIFISWSVPVAFGMIFELNFKGAEEIYYKHVHCRGG 190

QY 181 CSVFFSKISGVLTFMTSFYIPGSIIMLCVYRYIYLIAKEQARLISDANQ 228

Db 191 CSVFFSKISGVLTFMTSFYIPGSIIMLCVYRYIYLIAKEQARLISDANQ 238

RESULT 15

ABG93778

ID ABG93778 standard; protein; 238 AA.

XX AC ABG93778;

XX 26-NOV-2002 (first entry)

XX Human G protein-coupled receptor protein, nGPCR-seq56.

XX Human; receptor; G protein-coupled receptor; GPCR; nGPCR; nGPCR;
XX nGPCR protein coupled receptor; communication; serpentine structure;
XX seven transmembrane receptor; 7TM; mental disorder; diagnosis;
XX genetic predisposition; brain; immune response; gene therapy;
XX anxiety disorder; depression; bipolar disorder; schizophrenia;
XX Huntington's disease; dyskinesia; manic depression; stroke;
XX Parkinson's disease; Alzheimer's disease; diabetes; inflammation; wound;
XX tranquiliser.

XX Homo sapiens.

XX WO200264789-A1.

XX 22-AUG-2002.

XX 14-FEB-2001; 2001WO-US004641.

XX 14-FEB-2001; 2001WO-US004641.

XX (PHAA) PHARMACIA & UPJOHN CO.

XX Lind P, Parodi LA, Vogeli G, Wood LS;

XX WPI; 2002-674879/72.

XX N-PSDB; ABS70233.

XX New nucleic acids and polypeptides of the nGPCR protein-coupled receptor,
XX useful for treating or diagnosing a mental disorder or a disorder
XX affecting the brain, e.g. anxiety disorders, schizophrenia, stroke or
XX Parkinson's disease.

XX Example 1; Page 81; 244pp; English.

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OM protein - protein search, using sw model

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(without alignments)
969.421 Million cell updates/sec

Title: US-09-633-145-2
Perfect score: 1801
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/2/iaa/5B-COMB.pep:*
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4: /cgn2_6/ptodata/2/iaa/6B-COMB.pep:*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	813.5	45.2	343	2	US-08-788-539A-2
2	782	43.4	338	3	US-09-286-805-4
3	743	41.3	348	3	US-09-286-805-2
4	677.5	37.6	337	2	US-08-467-559B-2
5	534	29.7	360	4	US-09-555-313B-4
6	534	29.7	380	4	US-09-555-313B-24
7	534	29.7	388	1	US-08-446-822-8
8	534	29.7	388	4	US-09-328-314-8
9	534	29.7	388	5	PCT-US93-12586-8
10	534	29.7	760	4	US-09-555-313B-2
11	529	29.4	387	1	US-07-996-772A-2
12	529	29.4	387	1	US-08-446-822-2
13	529	29.4	387	4	US-09-328-314-2
14	529	29.4	387	5	PCT-US93-12586-2
15	529	29.4	406	4	US-09-328-314-4
16	527	29.3	406	1	US-07-996-772A-4
17	527	29.3	406	1	US-08-446-822-4
18	527	29.3	406	5	PCT-US93-12586-4
19	486	27.0	358	2	US-08-748-485-6
20	478.5	26.6	376	1	US-07-817-920-5
21	478.5	26.6	376	1	US-08-117-006-5
22	478.5	26.6	376	1	US-08-216-594-5
23	478.5	26.6	376	5	PCT-US93-00149-5
24	477.5	26.5	375	1	US-08-370-542-5
25	477.5	26.5	375	1	US-08-542-358-5
26	477.5	26.5	375	3	US-09-018-351-5
27	474.5	26.3	359	3	US-08-875-540-15
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					Sequence 24, Appli
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					Sequence 5, Appli
					Sequence 5, Appli
					Sequence 15, Appli

28 474.5 26.3 359 4 US-09-473-634-15 Sequence 15, Appli
29 474 26.3 377 2 US-08-461-812-2 Sequence 2, Appli
30 474 26.3 377 3 US-08-157-185-14 Sequence 14, Appli
31 474 26.3 377 3 US-08-281-526B-14 Sequence 14, Appli
32 474 26.3 377 4 US-09-450-790A-14 Sequence 14, Appli
33 474 26.3 377 4 US-09-332-837-14 Sequence 14, Appli
34 474 26.3 377 4 US-09-371-705-2 Sequence 2, Appli
35 472.5 26.2 359 2 US-08-467-568-13 Sequence 13, Appli
36 472.5 26.2 359 2 US-08-748-485-4 Sequence 2, Appli
37 472.5 26.2 359 2 US-08-103-170-2 Sequence 2, Appli
38 472.5 26.2 359 2 US-09-030-582-13 Sequence 13, Appli
39 472.5 26.2 359 4 US-09-171-456-19 Sequence 19, Appli
40 461.5 25.6 348 3 US-08-875-540-13 Sequence 13, Appli
41 461.5 25.6 348 4 US-09-171-456-17 Sequence 17, Appli
42 461.5 25.6 348 4 US-09-473-634-13 Sequence 13, Appli
43 459.5 25.5 359 2 US-08-748-485-5 Sequence 5, Appli
44 458 25.4 446 1 US-07-626-618A-21 Sequence 21, Appli
45 458 25.4 446 1 US-08-333-977-21 Sequence 21, Appli

ALIGNMENTS

RESULT 1
US-08-788-539A-2
; Sequence 2, Application US/08788539A
; Patent No. 5871967
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham Corporation
; TITLE OF INVENTION: CLONING OF A NOVEL G-PROTEIN
; TITLE OF INVENTION: COUPLED 7TM RECEPTOR
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/788.539A
; FILING DATE: 24-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Han, William T
; REGISTRATION NUMBER: 34,344
; REFERENCE/DOCKET NUMBER: ATGS0047
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5219
; TELEFAX: 610-270-4026
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 343 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-788-539A-2

Query Match 45.2%; Score 813.5; DB 2; Length 343;
Best Local Similarity 46.0%; Pred. No. 7.3e-64;
Matches 159; Conservative 57; Mismatches 99; Indels 31; Gaps 5;

QY 4 CHNIIN-----ISCVKNN-----WSNDVRASLYSLMVLIIITLVLGNLIVIVSISH 49

Db 13 CPKFNKILSSHQPIFSCPGDNVFGDWSHDY-----PFGNLIWVWISH 58
QY 50 FQKLTPTNWLHSMATVDFLLGCLVMPYSWVRSAEHCWYFGEVFCIKHTSTDMILSSAS 109
Db 59 FQKLSPTNWLHSMATVDFLLGCLVMPYSWVRSAEHCWYFGEVFCIKHTSTDMILSSAS 118
QY 110 IFHLSFISIDRYAVCDPLRYKAKMNLVLCVMIFISWVPAVAFGMIFLELNFPGARE 169
Db 119 IFHLSFISIDRYAVCDPLRYKAKMNLVLCVMIFISWVPAVAFGMIFLELNFPGARE 178
QY 170 IYKWHVCHRCGGSVPFSGKSLGVLTFMTSPYIPGSMILCVYRIYLIAXEQARLISDANOK 229
Db 179 -YKILVACENFALFENKFWGILFTTCFTGSGMWGIVGKLFIVSKOHARVISHPEN 237
QY 230 LQIGLEMKNGISQSKERKAVKTLGIVMGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLI 289
Db 238 TKGA--VKKHLSKKDKAKAATLGIWGVFLACWLPCLFLAVLIDPVLIDYSTPILILDILV 295
QY 290 WFGYLNSTENPMVYAFYFWRKALWMLFGKIFQKDSRCKLFLE 335
Db 296 WURYFNSTCNPLHGFNFQAFKFIIVSGKIFSHSETANLFE 341

RESULT 2

US-09-286-805-4
; Sequence 4, Application US/09286805
; Patent No. 6117990
; GENERAL INFORMATION:
; APPLICANT: Bonini, James A.
; APPLICANT: Borowsky, Beth E.
; TITLE OF INVENTION: DNA Encoding Orphan SNORF1 Receptor
; FILE REFERENCE: 58987
; CURRENT APPLICATION NUMBER: US/09/286,805
; CURRENT FILING DATE: 1999-04-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent In Ver. 2.0 - beta
; SEQ ID NO 4
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-286-805-4
Query Match 43.4%; Score 782; DB 3; Length 338;
Best Local Similarity 45.8%; Pred. No. 4.2e-61;
Matches 154; Conservative 63; Mismatches 115; Indels 4; Gaps 4;

QY 1 MPFCHNIINISCVXNNWSDVRASLYSLMVLHILITLVGNLIVIVSISHFKQLHTPTNWL 60
Db 1 MELCVENVNGSCIKSSYSPWRALVAVLGLGALLAVFGNLLVITALLHFKQLHTPTNWL 60
QY 61 IHSMATVDFLLGCLVMPYSWVRSAEHCWYFGEVFCIKHTSTDMILSSASIFHLSFISIDR 120
Db 61 VASLACADFLVGVTVMPFSTVRSVSGVCSWYFGEVFCIKHTSTDMILSSASIFHLSFISIDR 120
QY 121 YVAVCDPLRYKAKMNLVLCVMIFISWVPAVAFGMIFLELNFPGAREIYKWHVCHRCG 180
Db 121 YVAVCDPLRYKAKMNLVLCVMIFISWVPAVAFGMIFLELNFPGAREIYKWHVCHRCG 179
QY 181 CSVFFSKISGVLTFTMTSPYIPGSMILCVYRIYLIAXEQARLI-SDANOKLQIGLEMKNG 239
Db 180 CQAPLNQNVLLCFLL-FELPTVMVFLYGRIFLVAQKQARKIEGSANQPQASSESYKER 238
QY 240 ISQSKERKAVKTLGIVMGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTN 299
Db 239 VAR-RERKAAKTGLGIAAAFLVSWLPYIIDAVIDAYMNFITPAYVYVYELLVWCVYNSAMN 297
QY 300 PMVYAFYFWRKALWMLFGKIFQKDSRCKLFLE 335
Db 298 PLIYAFYFWRKALWMLFGKIFQKDSRCKLFLE 333

RESULT 3

US-09-286-805-2
; Sequence 2, Application US/09286805
; Patent No. 6117990
; GENERAL INFORMATION:
; APPLICANT: Bonini, James A.
; APPLICANT: Borowsky, Beth E.
; TITLE OF INVENTION: DNA Encoding Orphan SNORF1 Receptor
; FILE REFERENCE: 58987
; CURRENT APPLICATION NUMBER: US/09/286,805
; CURRENT FILING DATE: 1999-04-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent In Ver. 2.0 - beta
; SEQ ID NO 2
; LENGTH: 348
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-286-805-2
Query Match 41.3%; Score 743; DB 3; Length 348;
Best Local Similarity 42.5%; Pred. No. 1.2e-57;
Matches 141; Conservative 63; Mismatches 126; Indels 2; Gaps 2;

QY 4 CHNIINISCVXNNWSDVRASLYSLMVLHILITLVGNLIVIVSISHFKQLHTPTNWLHLS 63
Db 14 CYKNVNESCIKTPYSPGPRSIYAVLGFAGVLAAGNLLVMIALLHFKQLHTPTNFLIAS 73
QY 64 MATVDFLLGCLVMPYSWVRSAEHCWYFGEVFCIKHTSTDMILSSASIFHLSFISIDRYA 123
Db 74 LACADFLVGVTVMPFSTVRSVSGVCSWYFGEVFCIKHTSTDMILSSASIFHLSFISIDRYA 133
QY 124 VCDPLRYKAKMNLVLCVMIFISWVPAVAFGMIFLELNFPGAREIYKWHVCHRCGCSV 183
Db 134 VTDPITYPTKFTIVSGVCSWYFGEVFCIKHTSTDMILSSASIFHLSFISIDRYA 192
QY 184 FFSKISGVLTFTMTSPYIPGSMILCVYRIYLIAXEQARLI-SDANOKLQIGLEMKNGIS 243
Db 193 PLNQNVLLCFLL-FEIPNVAMVFIYKIFLVAQKQARKIEGSANQPQASSESYKERVAK 251
QY 244 KERKAVKTLGIVMGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTENPMVY 303
Db 252 RERKAAKTGLGIAAAFLVSWLPYIIDAVIDAYMNFITPAYVYVYELLVWCVYNSAMNPLIY 311
QY 304 AFFYFWRKALWMLFGKIFQKDSRCKLFLE 335
Db 312 AFFYFWRKALWMLFGKIFQKDSRCKLFLE 343

RESULT 4

US-08-467-559B-2
; Sequence 2, Application US/08467559B
; Patent No. 5928890
; GENERAL INFORMATION:
; APPLICANT: LI, YI
; TITLE OF INVENTION: HUMAN AMINE RECEPTOR
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN AND FOX, P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,559B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K


```

? TITLE OF INVENTION: DNA Encoding 5-HT4 Serotonin Receptors And Uses Thereof
?
? FILE REFERENCE: 42667-AZ-PCR-US
?
? CURRENT APPLICATION NUMBER: US/09/328,314
?
? CURRENT FILING DATE: 1998-04-03
?
? EARLIER APPLICATION NUMBER: 08/446,822
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? EARLIER FILING DATE: 1995-07-31
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? EARLIER APPLICATION NUMBER: PCT/US93/12586
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? EARLIER FILING DATE: 1993-12-22
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? EARLIER APPLICATION NUMBER: 07/996,772
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? EARLIER FILING DATE: 1992-12-24
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? NUMBER OF SEQ ID NOS: 19
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? SOFTWARE: PatentIn Ver. 2.1
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? SEQ ID NO 8
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? LENGTH: 388
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? TYPE: PRT
?
? ORGANISM: Homo sapiens
?
US-09-328-314-8

Query Match      29.7%; Score 534; DB 4; Length 388;
Best Local Similarity 37.4%; Pred. No. 3e-39;
Matches 116; Conservative 53; Mismatches 121; Indels 20; Gaps 5

QY 25 LYSIMVLIIITLGVNLIVIVISISHFKOLH-TPTNWLHSMATYDFLLGCLVMPYSWYRS 83
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 22 LLTFLSVIIMLGNLNLVNVAVCWDRQLRKIKTNFYIVSLAFADLLVSVLWMPFGALE 81
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 84 AEHCWFYEGVEFCIKHTSTDIMLSSASIFHLISFISIDRYAV-CDPLRYKAGNNILVICVM 142
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 82 VQDIWIYGEVFCIVRTSLDVLITASIFHLCCISLDRYAICCPLYVRNKNWTELRALM 141
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 143 IFISWSVPVAFQGMIFLEINFLNFKGAEIYYKHKVHCRGG----CSVFFSKISGVLTFTMTSF 198
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 142 LGGCGWIPTISFLPINQGMNNIGIIDLIEKRKFNQNSNSTYCFVMYMKPVAITCSVVAF 201
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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QY 199 IIFGSIIMLCVIFKILLIARQAKLISUWNAUQIGLEFNKNGISUS-----KRNKA 249
Db 202 YIIFLLMVLAYYRIYVTAKSHAHQI-----QWLOPAGASSESRPOSADQHSTHRMRTETKA 257
QY 249 VKTLGIWVGVLICWCPFEFICTVMDPFLHVIIPPTLNDVLIIWFGYLNSTENPMVYAPFP 308
Db 258 AKTLCIIMGFCICWAPFFVTNIVDPIDYTPGQVWTAFLWLGIYNSGLNPFYIAPLANK 317
QY 309 WFRKALMMML 318
Db 318 SFRAFLIIL 327

RESULT 9
PCT-US93-12586-8
; Sequence 8, Application PC/TUS9312586
; GENERAL INFORMATION:
; APPLICANT: SYNAPTIC PHARMACEUTICAL CORPORATION
; TITLE OF INVENTION: DNA ENCODING 5-HT4 SEROTONIN RECEPTORS
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOPER & DUNHAM
; STREET: 30 ROCKEFELLER PLAZA
; CITY: NEW YORK
; STATE: NEW YORK
; ZIP: 10112
; COMPUTER READABLE FORM:

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COMPUTER: IBM PC COMPACT
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/12586
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: White, P., John
REGISTRATION NUMBER: 28.678


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; REFERENCE/DOCKET NUMBER: 42667-A-PCT/JPW/TEP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 388 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US93-12586-8

Query Match 29.7%; Score 534; DB 5; Length 388;
Best Local Similarity 37.4%; Pred. No. 3e-39;
Matches 116; Conservative 53; Mismatches 121; Indels 20; Gaps 5;

QY 25 LYSMLVLIILTLVGNLIVIVISISHFKQLH-TPTNWLHSMATVDFLLGCLVMPYSMVRS 83
DB 22 LTLFSLTVILMAILGNLLVMVAVCDRLRKIKTNFYIVSLAFADLLVSLVMPFGAIEL 81
QY 84 AEHCWYFGEVFCIKHTSDIMLSSASIFHLSFISIDRYAV-CDPLRYKAKNNILVICM 142
DB 82 VQDIWIYGEVFCVLRVTSLDVLLTTASIFHLCCISLDRYVAICQPLVYRNKMTPLRIALM 141
QY 143 IFISWSVPAVAFGMIFLELNFKGAEIYYKHVHCRGG-----CSVFFSKISGLVTFMTSF 198
DB 142 LGGCWVIPTFISFLPMQGNNGIIDLIERKFNQNSNSTYCVPMVANKPYAITCSVVAF 201
QY 199 YIPGSIMLCVYVRYLIAKEQARLISDANQKLIQIGLEMKNGISQS-----KERKA 248
DB 202 YIPFLMLVLAIRIYVTAKEHAHQI-----QMLQAGASESRPQADQHSHTRMETETKA 257
QY 249 VKTLIGVMGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLIMFGYLNSTFNMVYAFYFP 308
DB 258 AKTLCIINGCFCLWAPFFVNIIVDPFDIDYTPGQVWTAFLMWGLYNSGLNPFYAFNLK 317
QY 309 WFRKALKMML 318
DB 318 SFRRFLIIL 327

RESULT 10
US-09-555-313B-2
; Sequence 2, Application US/09555313B
; Patent No. 6506580
; GENERAL INFORMATION:
; APPLICANT: FICHSMEISTER, Rudolph et al.
; TITLE OF INVENTION: Splicing variants of the human serotonin receptor
; TITLE OF INVENTION: 5-HT4 and uses thereof, in particular for screening
; FILE REFERENCE: P06762US00/BAS
; CURRENT APPLICATION NUMBER: US/09/555,313B
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: FR 97/15037
; PRIOR FILING DATE: 1997-11-28
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin ver. 2.1
; SEQ ID NO 2
; LENGTH: 760
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-555-313B-2

Query Match 29.7%; Score 534; DB 4; Length 760;
Best Local Similarity 37.4%; Pred. No. 6.4e-39;
Matches 116; Conservative 53; Mismatches 121; Indels 20; Gaps 5;

QY 25 LYSMLVLIILTLVGNLIVIVISISHFKQLH-TPTNWLHSMATVDFLLGCLVMPYSMVRS 83
DB 22 LTLFSLTVILMAILGNLLVMVAVCDRLRKIKTNFYIVSLAFADLLVSLVMPFGAIEL 81
QY 84 AEHCWYFGEVFCIKHTSDIMLSSASIFHLSFISIDRYAV-CDPLRYKAKNNILVICM 142
DB 82 VQDIWIYGEVFCVLRVTSLDVLLTTASIFHLCCISLDRYVAICQPLVYRNKMTPLRIALM 141
QY 143 IFISWSVPAVAFGMIFLELNFKGAEIYYKHVHCRGG-----CSVFFSKISGLVTFMTSF 198
DB 142 LGGCWVIPTFISFLPMQGNNGIIDLIERKFNQNSNSTYCVPMVANKPYAITCSVVAF 201
QY 199 YIPGSIMLCVYVRYLIAKEQARLISDANQKLIQIGLEMKNGISQS-----KERKA 248
DB 202 YIPFLMLVLAIRIYVTAKEHAHQI-----QMLQAGASESRPQADQHSHTRMETETKA 257
QY 249 VKTLIGVMGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLIMFGYLNSTFNMVYAFYFP 308
DB 258 AKTLCIINGCFCLWAPFFVNIIVDPFDIDYTPGQVWTAFLMWGLYNSGLNPFYAFNLK 317
QY 309 WFRKALKMML 318
DB 318 SFRRFLIIL 327

RESULT 11
US-07-996-772A-2
; Sequence 2, Application US/07996772A
; Patent No. 5472866
; GENERAL INFORMATION:
; APPLICANT: Gerald, Christophe
; APPLICANT: Hartig, Paul R.
; APPLICANT: Branche, Theresa A.
; APPLICANT: Weinshank, Richard L.
; TITLE OF INVENTION: DNA ENCODING 5-HT4 SEROTONIN
; TITLE OF INVENTION: RECEPTORS AND USES THEREOF
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOPER & DUNHAM
; STREET: 30 ROCKEFELLER PLAZA
; CITY: NEW YORK
; STATE: NEW YORK
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/996,772A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, P., John
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 42667/JPW/TEP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 387 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-996-772A-2

Query Match 29.4%; Score 529; DB 1; Length 387;
Best Local Similarity 35.4%; Pred. No. 8.3e-39;
Matches 111; Conservative 61; Mismatches 114; Indels 28; Gaps 6;

QY 25 LYSMLVLIILTLVGNLIVIVISISHFKQLH-TPTNWLHSMATVDFLLGCLVMPYSMVRS 83
DB 22 LTLFAMVILMAILGNLLVMVAVCDRLRKIKTNFYIVSLAFADLLVSLVNAFGAIEL 81
QY 84 AEHCWYFGEVFCIKHTSDIMLSSASIFHLSFISIDRYAV-CDPLRYKAKNNILVICM 142
DB 82 VQDIWIYGEVFCVLRVTSLDVLLTTASIFHLCCISLDRYVAICQPLVYRNKMTPLRIALM 141
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QY 143 IFISWSVAVFAFGMIFLELNFKGAEIY----YKHVHCRGCSVFFFSKISGVLFTMTSF 198
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QY 199 YIPGSIMLCVYRIYLIYIAKEOARLISDANKLOIGLEMKNGISQSK-----244
Db 202 YIPFLLMVLAYRIYVTAKEHA-----QQIQM-LQRAGATSESRPQTADQSHTRMT 253
QY 245 ERKAVKTLGIVMGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLWFGYLNSTFPMVYA 304
Db 254 ETAAKTLGVINGCFWCFWAPFFVTNIVDPFDITYVPEKVTAFWLWGLYNSGLNPLFYA 313
QY 305 FFPWFRKALKMML 318
Db 314 FLNKSFRRAFLIIL 327

RESULT 12

US-08-446-822-2
; Sequence 2, Application US/08446822
; Patent No. 5766879
; GENERAL INFORMATION:
; APPLICANT: SYNAPTIC PHARMACEUTICAL CORPORATION
; TITLE OF INVENTION: DNA ENCODING 5-HT4 SEROTONIN RECEPTORS
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOPER & DUNHAM
; STREET: 30 ROCKEFELLER PLAZA
; CITY: NEW YORK
; STATE: NEW YORK
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,822
; FILING DATE: June 1, 1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: White, P., John
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 42667-A-PCT-US/JPW/WAT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 387 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-446-822-2

Query Match 29.4%; Score 529; DB 1; Length 387;
Best Local Similarity 35.4%; Pred. No. 8.3e-39;
Matches 111; Conservative 61; Mismatches 114; Indels 28; Gaps 6;
QY 25 LYSMLVLIITLVGNLIVIVSISHFKQLH-TPTNWLHSMATVDFLLGCLVMPYSWVRS 83
Db 22 LLTFPAMVILMAILGNLLVMVAVCDRLQRLKIKTYFIVSLAFADLLVSLVNAFGAIEL 81
QY 84 AEHCWYFGEVFCIKHTSDIMLSSASIFHLGFSISIDRYAV-CDPLRYKAKNNILVICW 142
Db 82 VQDIWFYGEMLCVRTSLDVLTTASIFHLCCISLDRYAICCCQPLVYRNKMTPLRIALM 141
QY 143 IFISWSVAVFAFGMIFLELNFKGAEIY----YKHVHCRGCSVFFFSKISGVLFTMTSF 198
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QY 245 ERKAVKTLGIVMGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLWFGYLNSTFPMVYA 304
Db 254 ETAAKTLGVINGCFWCFWAPFFVTNIVDPFDITYVPEKVTAFWLWGLYNSGLNPLFYA 313
QY 305 FFPWFRKALKMML 318
Db 314 FLNKSFRRAFLIIL 327

RESULT 14

PCT-US93-12586-2
; Sequence 2, Application PC/TUS9312586
; GENERAL INFORMATION:

QY 199 YIPGSIMLCVYRIYLIYIAKEOARLISDANKLOIGLEMKNGISQSK-----244
Db 202 YIPFLLMVLAYRIYVTAKEHA-----QQIQM-LQRAGATSESRPQTADQSHTRMT 253
QY 245 ERKAVKTLGIVMGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLWFGYLNSTFPMVYA 304
Db 254 ETAAKTLGVINGCFWCFWAPFFVTNIVDPFDITYVPEKVTAFWLWGLYNSGLNPLFYA 313
QY 305 FFPWFRKALKMML 318
Db 314 FLNKSFRRAFLIIL 327
RESULT 13
US-09-328-314-2
; Sequence 2, Application US/09328314
; Patent No. 6331401
; GENERAL INFORMATION:
; APPLICANT: Gerald, Christophe
; APPLICANT: Branchek, Theresa
; APPLICANT: Weinshank, Richard L.
; TITLE OF INVENTION: DNA Encoding 5-HT4 Serotonin Receptors And Uses Thereof
; FILE REFERENCE: 42667-AZ-PCT-US
; CURRENT APPLICATION NUMBER: US/09/328,314
; CURRENT FILING DATE: 1998-04-03
; EARLIER APPLICATION NUMBER: 08/446,822
; EARLIER FILING DATE: 1995-07-31
; EARLIER APPLICATION NUMBER: PCT/US93/12586
; EARLIER FILING DATE: 1993-12-22
; EARLIER APPLICATION NUMBER: 07/996,772
; EARLIER FILING DATE: 1992-12-24
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-328-314-2

Query Match 29.4%; Score 529; DB 4; Length 387;
Best Local Similarity 35.4%; Pred. No. 8.3e-39;
Matches 111; Conservative 61; Mismatches 114; Indels 28; Gaps 6;

QY 25 LYSMLVLIITLVGNLIVIVSISHFKQLH-TPTNWLHSMATVDFLLGCLVMPYSWVRS 83
Db 22 LLTFPAMVILMAILGNLLVMVAVCDRLQRLKIKTYFIVSLAFADLLVSLVNAFGAIEL 81
QY 84 AEHCWYFGEVFCIKHTSDIMLSSASIFHLGFSISIDRYAV-CDPLRYKAKNNILVICW 142
Db 82 VQDIWFYGEMLCVRTSLDVLTTASIFHLCCISLDRYAICCCQPLVYRNKMTPLRIALM 141
QY 143 IFISWSVAVFAFGMIFLELNFKGAEIY----YKHVHCRGCSVFFFSKISGVLFTMTSF 198
Db 142 LGGCWVPMFISFLPMQWNNIGIVDIEKRFKNHNSNFCFVPMWNAFYAITCSVAVF 201
QY 199 YIPGSIMLCVYRIYLIYIAKEOARLISDANKLOIGLEMKNGISQSK-----244
Db 202 YIPFLLMVLAYRIYVTAKEHA-----QQIQM-LQRAGATSESRPQTADQSHTRMT 253
QY 245 ERKAVKTLGIVMGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLWFGYLNSTFPMVYA 304
Db 254 ETAAKTLGVINGCFWCFWAPFFVTNIVDPFDITYVPEKVTAFWLWGLYNSGLNPLFYA 313
QY 305 FFPWFRKALKMML 318
Db 314 FLNKSFRRAFLIIL 327

RESULT 14

PCT-US93-12586-2
; Sequence 2, Application PC/TUS9312586
; GENERAL INFORMATION:

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RESULT 15
US-09-328-314-4
; Sequence 4, Application US/09328314
; Patent No. 6331401
; GENERAL INFORMATION:
; APPLICANT: Gerald, Christophe
; APPLICANT: Hartig, Paul R.
; APPLICANT: Brancheck, Theresa
; APPLICANT: Weinshank, Richard L.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 8, 2004, 10:20:11 : Search time 130 Seconds
(without alignments)
836.678 Million cell updates/sec

Title: US-09-633-145-2

Perfect score: 1801

Sequence: 1 MPFCHNIINISCVKNWSD.....FGKIFQKDSRCKLFLELSS 338

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1351062 seqs, 321799191 residues

Total number of hits satisfying chosen parameters: 1351062

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications AA:*

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- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pdb.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1801	100.0	339	10	US-09-782-974C-90
3	1801	100.0	339	10	US-09-995-225-12
4	1801	100.0	339	14	US-10-267-217-6
5	1801	100.0	339	14	US-10-225-567A-639
6	1801	100.0	339	15	US-10-085-198-190
7	1801	100.0	339	15	US-10-085-198-192
8	1801	100.0	339	15	US-10-085-198-200
9	1786	99.2	339	12	US-10-380-614-2
10	1786	99.2	339	16	US-10-769-131-2
11	1520	84.4	296	10	US-09-782-974C-88
12	1403	77.9	332	14	US-10-267-217-4
13	1393	77.3	332	12	US-10-380-614-4
14	1393	77.3	332	16	US-10-769-131-4
15	1207	67.0	238	10	US-09-782-974C-64

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17	848	47.1	351	9	US-09-474-696-2	Sequence 2, Appli
18	848	47.1	351	14	US-10-307-736-2	Sequence 2, Appli
19	815	45.3	306	14	US-10-225-567A-577	Sequence 577, App
20	813.5	45.2	343	9	US-09-742-869-2	Sequence 2, Appli
21	813.5	45.2	343	14	US-10-225-567A-579	Sequence 579, App
22	805.5	44.7	296	14	US-10-251-852-6	Sequence 6, Appli
23	743	41.3	348	14	US-10-225-567A-645	Sequence 645, App
24	718	39.9	345	14	US-10-230-007B-2	Sequence 2, Appli
25	718	39.9	345	16	US-10-647-982A-2	Sequence 2, Appli
26	715	39.7	345	9	US-09-995-225-10	Sequence 10, Appli
27	715	39.7	345	10	US-09-782-974C-84	Sequence 84, Appli
28	715	39.7	345	10	US-09-995-225-10	Sequence 10, Appli
29	715	39.7	345	14	US-10-225-567A-685	Sequence 685, App
30	715	39.7	345	14	US-10-251-852-2	Sequence 2, Appli
31	715	39.7	345	15	US-10-085-198-196	Sequence 196, App
32	696	38.6	342	9	US-09-995-225-14	Sequence 14, Appli
33	696	38.6	342	10	US-09-791-932-118	Sequence 118, App
34	696	38.6	342	10	US-09-995-225-14	Sequence 14, Appli
35	696	38.6	342	14	US-10-225-567A-687	Sequence 687, App
36	696	38.6	342	15	US-10-232-798-998	Sequence 998, App
37	696	38.6	342	15	US-10-085-198-194	Sequence 194, App
38	694	38.5	342	14	US-10-330-220-2	Sequence 2, Appli
39	677.5	37.6	337	12	US-09-988-745-2	Sequence 2, Appli
40	677.5	37.6	337	14	US-10-180-946-2	Sequence 358, App
41	677.5	37.6	337	14	US-10-225-567A-358	Sequence 482, App
42	677.5	37.6	337	16	US-10-408-036-9	Sequence 9, Appli
43	675	37.5	332	16	US-10-398-036-9	Sequence 4, Appli
44	671.5	37.3	321	14	US-10-330-220-4	Sequence 5, Appli
45	671.5	37.3	321	14	US-10-251-852-5	

ALIGNMENTS

RESULT 1

US-09-995-225-12
; Sequence 12, Application US/09995225
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Chu, Zhi Liang
; APPLICANT: Dang, Huang T.
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Pride, Cameron
; TITLE OF INVENTION: Endogenous And No. US20020193584A1-Endogenous Versions of Human G
; FILE REFERENCE: AREN-0308
; CURRENT APPLICATION NUMBER: US/09/995,225
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: PCT/US99/23938
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/253,404
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/255,366
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/270,286
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/282,365
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/270,266
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/282,032
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,358
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,356
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/290,917
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 60/309,208

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; PRIOR FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 12
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. US20020193584A1el Sequence
US-09-995-225-12

Query Match      100.0%; Score 1801; DB 9; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.2e-156;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPFCHNIINISCVKNWNSNDVRASLYSLMVLIIITLTVGNLIVIVISISHFKQLHTPTNWL 60
Db 2 MPFCHNIINISCVKNWNSNDVRASLYSLMVLIIITLTVGNLIVIVISISHFKQLHTPTNWL 61
QY 61 IHSMATVDLLGCLVMPYSWVRSABHCWYFGEVFCCKIHTSTDIMLSSASIFHLSFISIDR 120
Db 62 IHSMATVDLLGCLVMPYSWVRSABHCWYFGEVFCCKIHTSTDIMLSSASIFHLSFISIDR 121
QY 121 YVAVCDPLRYKAKMNLIVICVMIFISWSVPVAFAGMIFLELNFKAEEIYYKHVHCRCG 180
Db 122 YVAVCDPLRYKAKMNLIVICVMIFISWSVPVAFAGMIFLELNFKAEEIYYKHVHCRCG 181
QY 181 CSVFPSKISGVLTFMTSFYIPGSIIMLCVYIRYLYIAKEQARLISDANKQLQIGLEMKNGI 240
Db 182 CSVFPSKISGVLTFMTSFYIPGSIIMLCVYIRYLYIAKEQARLISDANKQLQIGLEMKNGI 241
QY 241 SOSKERKAVKTLGIWGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTFNP 300
Db 242 SOSKERKAVKTLGIWGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTFNP 301
QY 301 MYVAFYFPWFRKALKXMLFGKIFQKDSRCKLFLELSS 338
Db 302 MYVAFYFPWFRKALKXMLFGKIFQKDSRCKLFLELSS 339

RESULT 2
US-09-782-974C-90
; Sequence 90, Application US/09782974C
; Publication No. US20030082534A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Lind, Peter
; APPLICANT: Wood, Linda S.
; APPLICANT: Parodi, Luis A.
; TITLE OF INVENTION: No. US20030082534A1el G Protein Coupled Receptor
; FILE REFERENCE: 411USPRM311
; CURRENT APPLICATION NUMBER: US/09/782,974C
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 60/165,838
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 09/714,449
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 60/198,568
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 60/166,071
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/166,678
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: 60/173,396
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/184,129
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/185,421
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/185,554
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/186,530
; PRIOR FILING DATE: 2000-03-02
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; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 90
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-782-974C-90

Query Match      100.0%; Score 1801; DB 10; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.2e-156;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPFCHNIINISCVKNWNSNDVRASLYSLMVLIIITLTVGNLIVIVISISHFKQLHTPTNWL 60
Db 2 MPFCHNIINISCVKNWNSNDVRASLYSLMVLIIITLTVGNLIVIVISISHFKQLHTPTNWL 61
QY 61 IHSMATVDLLGCLVMPYSWVRSABHCWYFGEVFCCKIHTSTDIMLSSASIFHLSFISIDR 120
Db 62 IHSMATVDLLGCLVMPYSWVRSABHCWYFGEVFCCKIHTSTDIMLSSASIFHLSFISIDR 121
QY 121 YVAVCDPLRYKAKMNLIVICVMIFISWSVPVAFAGMIFLELNFKAEEIYYKHVHCRCG 180
Db 122 YVAVCDPLRYKAKMNLIVICVMIFISWSVPVAFAGMIFLELNFKAEEIYYKHVHCRCG 181
QY 181 CSVFPSKISGVLTFMTSFYIPGSIIMLCVYIRYLYIAKEQARLISDANKQLQIGLEMKNGI 240
Db 182 CSVFPSKISGVLTFMTSFYIPGSIIMLCVYIRYLYIAKEQARLISDANKQLQIGLEMKNGI 241
QY 241 SOSKERKAVKTLGIWGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTFNP 300
Db 242 SOSKERKAVKTLGIWGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTFNP 301
QY 301 MYVAFYFPWFRKALKXMLFGKIFQKDSRCKLFLELSS 338
Db 302 MYVAFYFPWFRKALKXMLFGKIFQKDSRCKLFLELSS 339

RESULT 3
US-09-995-225-12
; Sequence 12, Application US/09995225
; Publication No. US20030139588A9
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Chu, Zhi Liang
; APPLICANT: Dang, Huang T.
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Pride, Cameron
; TITLE OF INVENTION: Endogenous And No. US20030139588A9-Endogenous Versions of Human G
; FILE REFERENCE: AREN-0308
; CURRENT APPLICATION NUMBER: US/09/995,225
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: PCT/US99/23938
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/253,404
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/255,366
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/270,286
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/282,365
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/270,266
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/282,032
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,358
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282,356
; PRIOR FILING DATE: 2001-04-06
```

; PRIOR APPLICATION NUMBER: 60/290,917
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 60/309,208
; PRIOR FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. US20030139588A9el Sequence
US-09-995-225-12

Query Match 100.0%; Score 1801; DB 10; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.2e-156;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPFCHNIINISCVKNNWSDVRASLYSLMVLIIITLVGNLIVIVISISHFKQLHTPTNWL 60
DB 2 MPFCHNIINISCVKNNWSDVRASLYSLMVLIIITLVGNLIVIVISISHFKQLHTPTNWL 61
QY 61 IHSMATVDFLLGCLVMPYSMVRSABHCWYFGEVFCIKHTSTDIMLSSASIFHLSFISIDR 120
DB 62 IHSMATVDFLLGCLVMPYSMVRSABHCWYFGEVFCIKHTSTDIMLSSASIFHLSFISIDR 121
QY 121 YYAVCDPLRYKAKNMILVICVMIFISWSVPVAFAGMIFLELNFPGAEIYYKHVHCRGG 180
DB 122 YYAVCDPLRYKAKNMILVICVMIFISWSVPVAFAGMIFLELNFPGAEIYYKHVHCRGG 181
QY 181 CSVFESKISGVLTFMTSFYIPGSIIMLCVYRYIYLIKAQEARLISDANQKQLIGLEMKNGI 240
DB 182 CSVFESKISGVLTFMTSFYIPGSIIMLCVYRYIYLIKAQEARLISDANQKQLIGLEMKNGI 241
QY 241 SOSKERKAVKTLGIYMGVFLICWCPPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTNP 300
DB 242 SOSKERKAVKTLGIYMGVFLICWCPPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTNP 301
QY 301 MYAFFYFWRKALKOMLFGKIFQKDSRCKLFLELSS 338
DB 302 MYAFFYFWRKALKOMLFGKIFQKDSRCKLFLELSS 339

RESULT 4
US-10-267-217-6
; Sequence 6, Application US/10267217
; Publication No. US20030105318A1
; GENERAL INFORMATION:
; APPLICANT: Borowsky, Beth E.
; APPLICANT: Gogozalek, Kristine L.
; APPLICANT: Jones, Kenneth A.
; TITLE OF INVENTION: DNA Encoding SNORF33 Receptor
; FILE REFERENCE: 59338A
; CURRENT APPLICATION NUMBER: US/10/267,217
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: US/09/413,433
; PRIOR FILING DATE: 1999-10-06
; PRIOR APPLICATION NUMBER: 09/322,257
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.0 - beta
; SEQ ID NO 6
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-267-217-6

Query Match 100.0%; Score 1801; DB 14; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.2e-156;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPFCHNIINISCVKNNWSDVRASLYSLMVLIIITLVGNLIVIVISISHFKQLHTPTNWL 60
DB 2 MPFCHNIINISCVKNNWSDVRASLYSLMVLIIITLVGNLIVIVISISHFKQLHTPTNWL 61
QY 61 IHSMATVDFLLGCLVMPYSMVRSABHCWYFGEVFCIKHTSTDIMLSSASIFHLSFISIDR 120
DB 62 IHSMATVDFLLGCLVMPYSMVRSABHCWYFGEVFCIKHTSTDIMLSSASIFHLSFISIDR 121
QY 121 YYAVCDPLRYKAKNMILVICVMIFISWSVPVAFAGMIFLELNFPGAEIYYKHVHCRGG 180
DB 122 YYAVCDPLRYKAKNMILVICVMIFISWSVPVAFAGMIFLELNFPGAEIYYKHVHCRGG 181
QY 181 CSVFESKISGVLTFMTSFYIPGSIIMLCVYRYIYLIKAQEARLISDANQKQLIGLEMKNGI 240
DB 182 CSVFESKISGVLTFMTSFYIPGSIIMLCVYRYIYLIKAQEARLISDANQKQLIGLEMKNGI 241
QY 241 SOSKERKAVKTLGIYMGVFLICWCPPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTNP 300
DB 242 SOSKERKAVKTLGIYMGVFLICWCPPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTNP 301
QY 301 MYAFFYFWRKALKOMLFGKIFQKDSRCKLFLELSS 338
DB 302 MYAFFYFWRKALKOMLFGKIFQKDSRCKLFLELSS 339

DB 2 MPFCHNIINISCVKNNWSDVRASLYSLMVLIIITLVGNLIVIVISISHFKQLHTPTNWL 61
QY 61 IHSMATVDFLLGCLVMPYSMVRSABHCWYFGEVFCIKHTSTDIMLSSASIFHLSFISIDR 120
DB 62 IHSMATVDFLLGCLVMPYSMVRSABHCWYFGEVFCIKHTSTDIMLSSASIFHLSFISIDR 121
QY 121 YYAVCDPLRYKAKNMILVICVMIFISWSVPVAFAGMIFLELNFPGAEIYYKHVHCRGG 180
DB 122 YYAVCDPLRYKAKNMILVICVMIFISWSVPVAFAGMIFLELNFPGAEIYYKHVHCRGG 181
QY 181 CSVFESKISGVLTFMTSFYIPGSIIMLCVYRYIYLIKAQEARLISDANQKQLIGLEMKNGI 240
DB 182 CSVFESKISGVLTFMTSFYIPGSIIMLCVYRYIYLIKAQEARLISDANQKQLIGLEMKNGI 241
QY 241 SOSKERKAVKTLGIYMGVFLICWCPPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTNP 300
DB 242 SOSKERKAVKTLGIYMGVFLICWCPPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTNP 301
QY 301 MYAFFYFWRKALKOMLFGKIFQKDSRCKLFLELSS 338
DB 302 MYAFFYFWRKALKOMLFGKIFQKDSRCKLFLELSS 339

RESULT 5
US-10-225-567A-639
; Sequence 639, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 639
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-639

Query Match 100.0%; Score 1801; DB 14; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.2e-156;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPFCHNIINISCVKNNWSDVRASLYSLMVLIIITLVGNLIVIVISISHFKQLHTPTNWL 60
DB 2 MPFCHNIINISCVKNNWSDVRASLYSLMVLIIITLVGNLIVIVISISHFKQLHTPTNWL 61
QY 61 IHSMATVDFLLGCLVMPYSMVRSABHCWYFGEVFCIKHTSTDIMLSSASIFHLSFISIDR 120
DB 62 IHSMATVDFLLGCLVMPYSMVRSABHCWYFGEVFCIKHTSTDIMLSSASIFHLSFISIDR 121
QY 121 YYAVCDPLRYKAKNMILVICVMIFISWSVPVAFAGMIFLELNFPGAEIYYKHVHCRGG 180
DB 122 YYAVCDPLRYKAKNMILVICVMIFISWSVPVAFAGMIFLELNFPGAEIYYKHVHCRGG 181
QY 181 CSVFESKISGVLTFMTSFYIPGSIIMLCVYRYIYLIKAQEARLISDANQKQLIGLEMKNGI 240
DB 182 CSVFESKISGVLTFMTSFYIPGSIIMLCVYRYIYLIKAQEARLISDANQKQLIGLEMKNGI 241
QY 241 SOSKERKAVKTLGIYMGVFLICWCPPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTNP 300
DB 242 SOSKERKAVKTLGIYMGVFLICWCPPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTNP 301
QY 301 MYAFFYFWRKALKOMLFGKIFQKDSRCKLFLELSS 338
DB 302 MYAFFYFWRKALKOMLFGKIFQKDSRCKLFLELSS 339

RESULT 6
US-10-085-198-190
; Sequence 190, Application US/10085198
; Publication No. US20040009907A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook et al.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-279
; CURRENT APPLICATION NUMBER: 60/271,646
; PRIOR FILING DATE: 2001-02-25
; PRIOR FILING DATE: 2001-02-26
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/311,981
; PRIOR FILING DATE: 2001-08-13
; PRIOR FILING DATE: 2001-08-16
; PRIOR FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: 60/271,840
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/277,324
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/286,096
; PRIOR FILING DATE: 2001-04-21
; PRIOR APPLICATION NUMBER: 60/299,695
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/315,614
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/272,405
; PRIOR FILING DATE: 2001-02-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 653
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 190
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-085-198-190

Query Match 100.0%; Score 1801; DB 15; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.2e-156;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPFCHNIINISCVKXNWSNDVRASLYSLMVLIIITLVGNLIVIVISISHFKQLHTPTNWL 60
Db 2 MPFCHNIINISCVKXNWSNDVRASLYSLMVLIIITLVGNLIVIVISISHFKQLHTPTNWL 61

QY 61 IHSMATVDFLLGCLVMPYSWVRSABHCWYFGEVFCCKIHTSTDIMLSSASIFHLSTSIDR 120
Db 62 IHSMATVDFLLGCLVMPYSWVRSABHCWYFGEVFCCKIHTSTDIMLSSASIFHLSTSIDR 121

QY 121 YVAVCDPLRYKAKMNLIVICVMIFISWSVPVAFAGMIFLELNFKGAEIYYKHVHCRGG 180
Db 122 YVAVCDPLRYKAKMNLIVICVMIFISWSVPVAFAGMIFLELNFKGAEIYYKHVHCRGG 181

QY 181 CSVFSKISGLVTFTSFYIPGSIIMLCVYRYIYLIATKEQARLISDANKQLQIGLEWKNGI 240
Db 182 CSVFSKISGLVTFTSFYIPGSIIMLCVYRYIYLIATKEQARLISDANKQLQIGLEWKNGI 241

QY 241 SOSKERKAVKTLGIVMGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTNP 300
Db 242 SOSKERKAVKTLGIVMGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTNP 301

QY 301 MYAIFYFPWFRKALKOMLFGKIFQKDSRCKLFLLESS 338
Db 302 MYAIFYFPWFRKALKOMLFGKIFQKDSRCKLFLLESS 339

RESULT 7
US-10-085-198-192
; Sequence 192, Application US/10085198

Publication No. US20040009907A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook et al.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-279
; CURRENT APPLICATION NUMBER: US/10/085,198
; CURRENT FILING DATE: 2002-02-25
; PRIOR FILING DATE: 2001-02-26
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/271,646
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/311,981
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 60/312,858
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/271,840
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 60/277,324
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/286,096
; PRIOR FILING DATE: 2001-04-21
; PRIOR APPLICATION NUMBER: 60/299,695
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/315,614
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/272,405
; PRIOR FILING DATE: 2001-02-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 653
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 192
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-085-198-192

Query Match 100.0%; Score 1801; DB 15; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.2e-156;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPFCHNIINISCVKXNWSNDVRASLYSLMVLIIITLVGNLIVIVISISHFKQLHTPTNWL 60
Db 2 MPFCHNIINISCVKXNWSNDVRASLYSLMVLIIITLVGNLIVIVISISHFKQLHTPTNWL 61

QY 61 IHSMATVDFLLGCLVMPYSWVRSABHCWYFGEVFCCKIHTSTDIMLSSASIFHLSTSIDR 120
Db 62 IHSMATVDFLLGCLVMPYSWVRSABHCWYFGEVFCCKIHTSTDIMLSSASIFHLSTSIDR 121

QY 121 YVAVCDPLRYKAKMNLIVICVMIFISWSVPVAFAGMIFLELNFKGAEIYYKHVHCRGG 180
Db 122 YVAVCDPLRYKAKMNLIVICVMIFISWSVPVAFAGMIFLELNFKGAEIYYKHVHCRGG 181

QY 181 CSVFSKISGLVTFTSFYIPGSIIMLCVYRYIYLIATKEQARLISDANKQLQIGLEWKNGI 240
Db 182 CSVFSKISGLVTFTSFYIPGSIIMLCVYRYIYLIATKEQARLISDANKQLQIGLEWKNGI 241

QY 241 SOSKERKAVKTLGIVMGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTNP 300
Db 242 SOSKERKAVKTLGIVMGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTNP 301

QY 301 MYAIFYFPWFRKALKOMLFGKIFQKDSRCKLFLLESS 338
Db 302 MYAIFYFPWFRKALKOMLFGKIFQKDSRCKLFLLESS 339

RESULT 8
US-10-085-198-200
; Sequence 200, Application US/10085198
; Publication No. US20040009907A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook et al.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-279


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; CURRENT APPLICATION NUMBER: US/10/085,198
; CURRENT FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 60/271,646
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/276,401
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/311,981
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 60/312,858
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/271,840
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/277,324
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/286,096
; PRIOR FILING DATE: 2001-04-21
; PRIOR APPLICATION NUMBER: 60/299,695
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/315,614
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/272,405
; PRIOR FILING DATE: 2001-02-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 653
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 200
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-085-198-200

Query Match
Best Local Similarity 100.0%; Score 1801; DB 15; Length 339;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPFCHNIINISCVKNWSDVRASLYSLMVLIIITLVGNLIVIVSISHFKQLHTPTNWL 60
Db 2 MPFCHNIINISCVKNWSDVRASLYSLMVLIIITLVGNLIVIVSISHFKQLHTPTNWL 61
QY 61 IHSMATVDFLLGCLVMPYSWVSAEHCWYFGEVFCIKHTSTDMILSSAIFHLSPFISIDR 120
Db 62 IHSMATVDFLLGCLVMPYSWVSAEHCWYFGEVFCIKHTSTDMILSSAIFHLSPFISIDR 121
QY 121 YVAVCDPLRYKAKMNLIVICVMIFISWSVPVAFAGMIFLELNFKGAEEIYKXHVHCRGG 180
Db 122 YVAVCDPLRYKAKMNLIVICVMIFISWSVPVAFAGMIFLELNFKGAEEIYKXHVHCRGG 181
QY 181 CSVFFSKISGVLTFMTSFYIPGSIMLCVYRYLYIAKEQARLISDANQKIQIGLEMKNGI 240
Db 182 CLVFFSKISGVLTFMTSFYIPGSIMLCVYRYLYIAKEQARLISDANQKIQIGLEMKNGI 241
QY 241 SOSKERVAVKTLGIYVNGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTFNP 300
Db 242 SOSKERVAVKTLGIYVNGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTFNP 301
QY 301 MYAFYFPWFRKALXKMLFGKIFQKDSRCKLFLELSS 338
Db 302 MYAFYFPWFRKALXKMLFGKIFQKDSRCKLFLELSS 339

RESULT 9
US-10-380-614-2
; Sequence 2, Application US/10380614
; Publication No. US20040072187A1
; GENERAL INFORMATION:
; APPLICANT: Bunzow, James
; APPLICANT: Grandy, David
; TITLE OF INVENTION: Novel Mammalian Receptor Genes and Uses
; FILE REFERENCE: 98-520-E
; CURRENT APPLICATION NUMBER: US/10/380,614
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: US 09/659,519

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; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: PCT/US01/28455
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 60/303,967
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-380-614-2

Query Match
Best Local Similarity 99.2%; Score 1786; DB 12; Length 339;
Matches 336; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MPFCHNIINISCVKNWSDVRASLYSLMVLIIITLVGNLIVIVSISHFKQLHTPTNWL 60
Db 2 MPFCHNIINISCVKNWSDVRASLYSLMVLIIITLVGNLIVIVSISHFKQLHTPTNWL 61
QY 61 IHSMATVDFLLGCLVMPYSWVSAEHCWYFGEVFCIKHTSTDMILSSAIFHLSPFISIDR 120
Db 62 IHSMATVDFLLGCLVMPYSWVSAEHCWYFGEVFCIKHTSTDMILSSAIFHLSPFISIDR 121
QY 121 YVAVCDPLRYKAKMNLIVICVMIFISWSVPVAFAGMIFLELNFKGAEEIYKXHVHCRGG 180
Db 122 YVAVCDPLRYKAKMNLIVICVMIFISWSVPVAFAGMIFLELNFKGAEEIYKXHVHCRGG 181
QY 181 CSVFFSKISGVLTFMTSFYIPGSIMLCVYRYLYIAKEQARLISDANQKIQIGLEMKNGI 240
Db 182 CLVFFSKISGVLTFMTSFYIPGSIMLCVYRYLYIAKEQARLISDANQKIQIGLEMKNGI 241
QY 241 SOSKERVAVKTLGIYVNGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTFNP 300
Db 242 SOSKERVAVKTLGIYVNGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLIWFGYLNSTFNP 301
QY 301 MYAFYFPWFRKALXKMLFGKIFQKDSRCKLFLELSS 338
Db 302 MYAFYFPWFRKALXKMLFGKIFQKDSRCKLFLELSS 339

RESULT 10
US-10-769-131-2
; Sequence 2, Application US/10769131
; Publication No. US20040142390A1
; GENERAL INFORMATION:
; APPLICANT: Bunzow, James
; APPLICANT: Grandy, David
; TITLE OF INVENTION: Novel Mammalian Catecholamine Receptor Genes and Uses
; FILE REFERENCE: 98-520
; CURRENT APPLICATION NUMBER: US/10/769,131
; CURRENT FILING DATE: 2004-01-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-769-131-2

Query Match
Best Local Similarity 99.2%; Score 1786; DB 16; Length 339;
Matches 336; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MPFCHNIINISCVKNWSDVRASLYSLMVLIIITLVGNLIVIVSISHFKQLHTPTNWL 60
Db 2 MPFCHNIINISCVKNWSDVRASLYSLMVLIIITLVGNLIVIVSISHFKQLHTPTNWL 61
QY 61 IHSMATVDFLLGCLVMPYSWVSAEHCWYFGEVFCIKHTSTDMILSSAIFHLSPFISIDR 120
Db 62 IHSMATVDFLLGCLVMPYSWVSAEHCWYFGEVFCIKHTSTDMILSSAIFHLSPFISIDR 121

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QY 121 YYAVCDPLRYKAKMNLIVICVMIFISWSVPAVFAFGMIFLELNFKGABEIIYKXHVCRGG 180
 DB 122 YYAVCDPLRYKAKMNLIVICVMIFISWSVPAVFAFGMIFLELNFKGABEIIYKXHVCRGG 181
 QY 181 CSVFFSKISGVLTFMTSFYIPGIMLCVYRYIYLIYLAKEQARLISDANOKLQIGLEMKNGI 240
 DB 182 CLVFFSKISGVLTFMTSFYIPGIMLCVYRYIYLIYLAKEQARLISDANOKLQIGLEMKNGI 241
 QY 241 SOSKERRKAVKTLGIVMGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLWFGYLNSTFNP 300
 DB 242 SOSKERRKAVKTLGIVMGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLWFGYLNSTFNP 301
 QY 301 MYVAFYFPFRKALKMVLFGKIFQKDSRSRCKLFL 338
 DB 302 MYVAFYFPFRKALKMVLFGKIFQKDSRSRCKLFL 339

RESULT 11
 US-09-782-974C-88
 ; Sequence 88, Application US/09782974C
 ; Publication No. US20030082534A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Vogel, Gabriel
 ; APPLICANT: Lind, Peter
 ; APPLICANT: Wood, Linda S.
 ; APPLICANT: Parodi, Luis A.
 ; TITLE OF INVENTION: No. US20030082534A1 G Protein Coupled Receptor
 ; FILE REFERENCE: 411USPHRM311
 ; CURRENT APPLICATION NUMBER: US/09/782,974C
 ; CURRENT FILING DATE: 2002-09-04
 ; PRIOR APPLICATION NUMBER: 60/165,838
 ; PRIOR FILING DATE: 1999-11-16
 ; PRIOR APPLICATION NUMBER: 09/714,449
 ; PRIOR FILING DATE: 2000-11-16
 ; PRIOR APPLICATION NUMBER: 60/198,568
 ; PRIOR FILING DATE: 2000-04-20
 ; PRIOR APPLICATION NUMBER: 60/166,071
 ; PRIOR FILING DATE: 1999-11-17
 ; PRIOR APPLICATION NUMBER: 60/166,678
 ; PRIOR FILING DATE: 1999-11-19
 ; PRIOR APPLICATION NUMBER: 60/173,396
 ; PRIOR FILING DATE: 1999-12-28
 ; PRIOR APPLICATION NUMBER: 60/184,129
 ; PRIOR FILING DATE: 2000-02-22
 ; PRIOR APPLICATION NUMBER: 60/185,421
 ; PRIOR FILING DATE: 2000-02-28
 ; PRIOR APPLICATION NUMBER: 60/185,554
 ; PRIOR FILING DATE: 2000-02-28
 ; PRIOR APPLICATION NUMBER: 60/186,530
 ; PRIOR FILING DATE: 2000-03-02
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 192
 ; SOFTWARE: Patent in version 3.1
 ; SEQ ID NO 88
 ; LENGTH: 296
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-782-974C-88

Query Match 84.4%; Score 1520; DB 10; Length 296;
 Best Local Similarity 100.0%; Pred. No. 1.3e-130;
 Matches 286; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPFCHNIINISCVKNWSDVRASLYSLMVLIIITLVGNLIIVIVISHFQKLTHTPTNWL 60
 DB 2 MPFCHNIINISCVKNWSDVRASLYSLMVLIIITLVGNLIIVIVISHFQKLTHTPTNWL 61
 QY 61 IHSMATVDFLLGCLVMPYSWVSAEHCWYFGEVFCIKHTSTDMLSASIFHLSTFISIDR 120
 DB 62 IHSMATVDFLLGCLVMPYSWVSAEHCWYFGEVFCIKHTSTDMLSASIFHLSTFISIDR 121
 QY 121 YYAVCDPLRYKAKMNLIVICVMIFISWSVPAVFAFGMIFLELNFKGABEIIYKXHVCRGG 180

DB 122 YYAVCDPLRYKAKMNLIVICVMIFISWSVPAVFAFGMIFLELNFKGABEIIYKXHVCRGG 181
 QY 181 CSVFFSKISGVLTFMTSFYIPGIMLCVYRYIYLIYLAKEQARLISDANOKLQIGLEMKNGI 240
 DB 182 CSVFFSKISGVLTFMTSFYIPGIMLCVYRYIYLIYLAKEQARLISDANOKLQIGLEMKNGI 241
 QY 241 SOSKERRKAVKTLGIVMGVFLICWCPFFICTVMDPFLHYIIPPTLND 286
 DB 242 SOSKERRKAVKTLGIVMGVFLICWCPFFICTVMDPFLHYIIPPTLND 287

RESULT 12
 US-10-267-217-4
 ; Sequence 4, Application US/10267217
 ; Publication No. US20030105318A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Borowsky, Beth E.
 ; APPLICANT: Ogozalek, Kristine L.
 ; APPLICANT: Jones, Kenneth A.
 ; TITLE OF INVENTION: DNA Encoding SNORF33 Receptor
 ; FILE REFERENCE: 59338A
 ; CURRENT APPLICATION NUMBER: US/10/267,217
 ; CURRENT FILING DATE: 2002-10-07
 ; PRIOR APPLICATION NUMBER: US/09/413,433
 ; PRIOR FILING DATE: 1999-10-06
 ; PRIOR APPLICATION NUMBER: 09/322,257
 ; PRIOR FILING DATE: 1999-05-28
 ; NUMBER OF SEQ ID NOS: 35
 ; SOFTWARE: Patent in Ver. 2.0 - beta
 ; SEQ ID NO 4
 ; LENGTH: 332
 ; TYPE: PRT
 ; ORGANISM: Rattus norvegicus
 US-10-267-217-4

Query Match 77.9%; Score 1403; DB 14; Length 332;
 Best Local Similarity 78.1%; Pred. No. 7.3e-120;
 Matches 261; Conservative 27; Mismatches 44; Indels 2; Gaps 1;
 QY 1 MPFCHNIINISCVKNWSDVRASLYSLMVLIIITLVGNLIIVIVISHFQKLTHTPTNWL 60
 DB 1 MHLCHNSANISHTNSWSDVRASLYSLMVLIIITLVGNLIIVIVISHFQKLTHTPTNWL 60
 QY 61 IHSMATVDFLLGCLVMPYSWVSAEHCWYFGEVFCIKHTSTDMLSASIFHLSTFISIDR 120
 DB 61 LHSMAVDFLLGCLVMPYSWVSAEHCWYFGEVFCIKHTSTDMLSASIFHLSTFISIDR 120
 QY 121 YYAVCDPLRYKAKMNLIVICVMIFISWSVPAVFAFGMIFLELNFKGABEIIYKXHVCRGG 180
 DB 121 YYAVCDPLRYKAKINLAAIFVMIILISWSLPAVFAFGMIFLELNLEGVEELHYNQVFCRG 180
 QY 181 CSVFFSKISGVLTFMTSFYIPGIMLCVYRYIYLIYLAKEQARLISDANOKLQIGLEMKNGI 240
 DB 181 CFPFFSKVSGVLAFMTSFYIPGIMLCVYRYIYLIYLAKEQARLISDANOKLQIGLEMKNGI 238
 QY 241 SOSKERRKAVKTLGIVMGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLWFGYLNSTFNP 300
 DB 239 PQSKETKAAKTLGIMVGVFLLCWCPCFFFCWVLDPLFGYVIPPPTLNDTLNFWGYLNSAENP 298
 QY 301 MYVAFYFPFRKALKMVLFGKIFQKDSRSRCKLFL 334
 DB 299 MYVAFYFPFRKALKMVLFGKIFQKDSRSRCKLFL 332

RESULT 13
 US-10-380-614-4
 ; Sequence 4, Application US/10380614
 ; Publication No. US20040072187A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Oregon Health and Science University
 ; APPLICANT: Bunzow, James
 ; APPLICANT: Grandy, David
 ; TITLE OF INVENTION: Novel Mammalian Receptor Genes and Uses

```

; FILE REFERENCE: 98-520-E
; CURRENT APPLICATION NUMBER: US/10/380,614
; PRIOR FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: US 09/659,519
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: PCT/US01/28455
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 60/303,967
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 4
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-380-614-4

Query Match
Best Local Similarity 77.3%; Score 1393; DB 12; Length 332;
Matches 259; Conservative 27; Mismatches 46; Indels 2; Gaps 1;

QY 1 MPFCHNIINISCVKNWNSDVRASLYSLMVLIIITLVGNLIVIVISHSFKQLHTPTNWL 60
Db 1 MHLCHNSANISHTNRNWSRDRASLYSLIIITLVGNLIVIVISHSFKQLHTPTNWL 60
QY 61 IHSMATVDFLLGCLVMPYSWVSAEHCWYFGEVFCCKIHTSTDMILSSASIFHLSFISIDR 120
Db 61 LHSMAVDFLLGCLVMPYSWVSAEHCWYFGEVFCCKIHTSTDMILSSASILHLAFISIDR 120
QY 121 YVAVCDPLRYKAKMNLIVCMIFISWSVPVAFAGMIFELNFKGAEIYVYKHVHCRGG 180
Db 121 YVAVCDPLRYKAKINLAIFVMLISWSLPVAFAGMIFELNLEGVVEQYHNQVFCFLRG 180
QY 181 CSVPFSKISGVLTFTMTSFYIPGSIMLCVYRYIYLIKEQARLISDANQKIQIGLEMKNGI 240
Db 181 CFLFFSKVSGVLAFMTSFYIPGSVLMFVYIYFIYFIAGQARSINRAN--LOVLEGESRA 238
QY 241 SOSKERKAVKTLGIWVGVELICWCPFFICTVMDPFLHYIIPPTLNDVLWFGYLNSTFNP 300
Db 239 POSKETKAATLGIWVGVELLCWCPFFFCWLDPLFGYVIPPPTLNDTLNFWGFLNSAFNP 298
QY 301 MYAFYFPWFRKALXWMLFGKIFQKDSRSCKLFL 334
Db 299 MYAFYFPWFRALXWMLFGKIFQKDSRSCKLFL 332

RESULT 14
US-10-769-131-4
; Sequence 4, Application US/10769131
; Publication No. US20040142390A1
; GENERAL INFORMATION:
; APPLICANT: Bunzow, James
; APPLICANT: Grandy, David
; TITLE OF INVENTION: Novel Mammalian Catecholamine Receptor Genes and Uses
; CURRENT APPLICATION NUMBER: US/10/769,131
; CURRENT FILING DATE: 2004-01-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 4
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-769-131-4

Query Match
Best Local Similarity 77.3%; Score 1393; DB 16; Length 332;
Matches 259; Conservative 27; Mismatches 46; Indels 2; Gaps 1;

QY 1 MPFCHNIINISCVKNWNSDVRASLYSLMVLIIITLVGNLIVIVISHSFKQLHTPTNWL 60
Db 1 MHLCHNSANISHTNRNWSRDRASLYSLIIITLVGNLIVIVISHSFKQLHTPTNWL 60

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QY 61 IHSMATVDFLLGCLVMPYSWVSAEHCWYFGEVFCCKIHTSTDMILSSASIFHLSFISIDR 120
Db 61 LHSMAVDFLLGCLVMPYSWVSAEHCWYFGEVFCCKIHTSTDMILSSASILHLAFISIDR 120
QY 121 YVAVCDPLRYKAKMNLIVCMIFISWSVPVAFAGMIFELNFKGAEIYVYKHVHCRGG 180
Db 121 YVAVCDPLRYKAKINLAIFVMLISWSLPVAFAGMIFELNLEGVVEQYHNQVFCFLRG 180
QY 181 CSVPFSKISGVLTFTMTSFYIPGSIMLCVYRYIYLIKEQARLISDANQKIQIGLEMKNGI 240
Db 181 CFLFFSKVSGVLAFMTSFYIPGSVLMFVYIYFIYFIAGQARSINRAN--LOVLEGESRA 238
QY 241 SOSKERKAVKTLGIWVGVELICWCPFFICTVMDPFLHYIIPPTLNDVLWFGYLNSTFNP 300
Db 239 POSKETKAATLGIWVGVELLCWCPFFFCWLDPLFGYVIPPPTLNDTLNFWGFLNSAFNP 298
QY 301 MYAFYFPWFRKALXWMLFGKIFQKDSRSCKLFL 334
Db 299 MYAFYFPWFRALXWMLFGKIFQKDSRSCKLFL 332

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RESULT 15
US-09-782-974C-64
; Sequence 64, Application US/09782974C
; Publication No. US20030082534A1
; GENERAL INFORMATION:
; APPLICANT: Vogel, Gabriel
; APPLICANT: Lind, Peter
; APPLICANT: Wood, Linda S.
; APPLICANT: Parodi, Luis A.
; TITLE OF INVENTION: No. US20030082534A1el G Protein Coupled Receptor
; FILE REFERENCE: 411USPRM311
; CURRENT APPLICATION NUMBER: US/09/782,974C
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 60/165,838
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 09/714,449
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 60/198,568
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 60/166,071
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/166,678
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: 60/173,396
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/184,129
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/185,421
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/185,554
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/186,530
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 64
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-782-974C-64

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Query Match
Best Local Similarity 100.0%; Pred. No. 4.1e-102;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPFCHNIINISCVKNWNSDVRASLYSLMVLIIITLVGNLIVIVISHSFKQLHTPTNWL 60
Db 11 MPFCHNIINISCVKNWNSDVRASLYSLMVLIIITLVGNLIVIVISHSFKQLHTPTNWL 70
QY 61 IHSMATVDFLLGCLVMPYSWVSAEHCWYFGEVFCCKIHTSTDMILSSASIFHLSFISIDR 120

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Db 71 IHSMATVDELLCCLVMPYSWPSAEHCWYFGEVPCCKIHTSTDIMLSSASIFHLSPISDR 130
QY 121 YYAVCDPLRYKAKMNLVICVMIFISWSVPVAFAGMIFLELNFKAEEIYYKHVHCRGG 180
Db 131 YYAVCDPLRYKAKMNLVICVMIFISWSVPVAFAGMIFLELNFKAEEIYYKHVHCRGG 190
QY 181 CSVFPSKISGVLTFMTSFYIPGSIMLCVYRIYLIKEQARLISDANQ 228
Db 191 CSVFPSKISGVLTFMTSFYIPGSIMLCVYRIYLIKEQARLISDANQ 238

Search completed: October 8, 2004, 10:31:00
Job time : 132 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 8, 2004, 10:17:10 ; Search time 19 seconds
(without alignments)
1711.197 Million cell updates/sec

Title: US-09-633-145-2

Perfect score: 1801

Sequence: 1 MFPCNNIISCVKNWNSND.....FGKIFQKSSRCKLFLSLSS 338

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	677.5	37.6	337	2 JC5832	neurotransmitter r
2	529	29.4	387	2 S55550	5-HT4s receptor -
3	529	29.4	406	2 S55549	serotonin 4 recept
4	510.5	28.3	459	2 A56849	dopamine receptor-
5	497.5	27.6	465	2 I51661	dopamine D1C recep
6	493.5	27.4	363	2 I50475	dopamine D1 recep
7	486	27.0	358	2 J01278	histamine H2 recep
8	482	26.8	444	2 C55886	dopamine receptor
9	482	26.8	450	2 A55886	dopamine receptor
10	481	26.7	457	2 I51660	dopamine D1B recep
11	480	26.4	451	2 I51659	dopamine D1A recep
12	475	26.4	377	2 S68423	serotonin receptor
13	474	26.3	377	2 A53279	serotonin receptor
14	473	26.3	374	2 I77467	serotonin receptor
15	472.5	26.2	359	2 JH0449	serotonin receptor
16	467	25.9	446	2 I47217	dopamine H2 recep
17	466.5	25.9	377	2 B30341	dopamine receptor
18	466.5	25.9	386	2 S72168	G protein-coupled
19	462.5	25.7	463	2 B56849	dopamine receptor-
20	461	25.6	483	2 A25896	beta-adrenergic re
21	459.5	25.5	359	2 C4120	histamine H2 recep
22	458	25.4	446	1 DXHUD1	dopamine receptor
23	454.5	25.2	477	1 DXHUD5	dopamine receptor
24	452	25.1	418	1 QRHYB2	beta-2-adrenergic
25	451	25.0	418	2 S10855	beta-2-adrenergic
26	450.5	25.0	359	2 A39008	histamine H2 recep
27	450	25.0	475	2 A41271	dopamine receptor
28	449.5	25.0	464	2 S12591	beta-1-adrenergic
29	449	24.9	418	2 S00260	beta-2-adrenergic

30	446.5	24.8	415	2 I53040	beta-2 adrenergic
31	446.5	24.8	487	1 DYRTD1	dopamine receptor
32	446	24.8	466	2 S36794	beta-1-adrenergic
33	438.5	24.3	413	1 QRHUB2	beta-2-adrenergic
34	437.5	24.3	486	2 B55886	dopamine receptor
35	433.5	24.1	477	1 QRHUB1	beta-1-adrenergic
36	432.5	24.0	366	2 A47321	serotonin receptor
37	429.5	23.8	428	2 A55044	beta-4C-adrenergic
38	429	23.8	480	2 I53053	beta 1 adrenergic
39	427.5	23.7	366	2 S26048	serotonin receptor
40	427.5	23.7	386	2 A42688	serotonin receptor
41	427.5	23.7	386	2 S18637	serotonin receptor
42	427	23.7	477	2 S71323	alpha-1A adrenergi
43	425.5	23.6	429	2 S65656	alpha-1C-adrenergi
44	425.5	23.6	466	2 JN0765	alpha-1C-adrenergi
45	425.5	23.6	499	2 S65657	alpha-1C-adrenergi

ALIGNMENTS

RESULT 1

JC5832

neurotransmitter receptor - human

C:Species: Homo sapiens (man)

C>Date: 20-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 24-Nov-1999

C:Accession: JC5832

R:Zeng, Z.; Pan, P.; Rand, E.; Kyaw, H.; Su, K.; Madike, V.; Carter, K.C.; Li, Y.

A:Title: Cloning of a putative human neurotransmitter receptor expressed in skeletal mus

A:Reference number: JC5832; MUID:98125534; PMID:9464258

A:Accession: JC5832

A:Molecule type: mRNA

A:Residues: 1-337 <ZEN>

A:Cross-references: GB:AF021818; NID:G2465431; PIDN:AAC39581.1; PID:G2465432

A:Experimental source: brain

C:Genetics:

A:Map position: 6q23

C:Superfamily: vertebrate rhodopsin

C:Keywords: glycoprotein; receptor; transmembrane protein

F:29-63/Domain: transmembrane #status predicted <TM1>

F:69-95/Domain: transmembrane #status predicted <TM2>

F:114-118/Domain: transmembrane #status predicted <TM3>

F:149-173/Domain: transmembrane #status predicted <TM4>

F:186-200/Domain: transmembrane #status predicted <TM5>

F:204-229/Domain: transmembrane #status predicted <TM6>

F:253-310/Domain: transmembrane #status predicted <TM7>

F:21/Binding site: carbohydrate (Asn) #status predicted

Query Match 37.6%; Score 677.5; DB 2; Length 337;

Best Local Similarity 39.0%; Pred. No. 3.2e-49;

Matches 130; Conservative 67; Mismatches 125; Indels 11; Gaps 4;

QY	3	FCHNIINISCVKNWNSNDVRA	SLVLIITLTVGNLIVIVSIS	HEKQLHTPTNWLH	62
Db	16	FCYQ-VNGSCRTVHTLGIQ	VLITCAAGMLIIVLGNVFA	VAVSYFKAHTPTNFLLL	74
QY	63	SNATVDFLLGCLVMPYSMV	RSAEHCWYGEVFCIKHTST	DIIMLSSAFHLSFISIDRY	122
Db	75	SLALADMFLLGLVLPSTIR	SVESCWFGDFLCRLHTVLD	TLFCLTSIFHLCFISIDRHC	134
QY	123	AVCDPLRYKAKNNILVICV	MFISNSVPAVAFGMIFELN	PKGAEEIYYKHVHCRGGS	182
Db	135	AICDPLLYPSFTVRVALRY	ILAGMGVPAAYTSFLYTDV	VVETRLSQ-WLEEMPCVGS	193
QY	183	VFFSKISGLVTFMTSFYIP	GSIMLCVYVRIYLIKEQAR	LISDANQKLIQIGLEKNGIS	242
Db	194	LLLKNFQWLNFP-PLFFV	PCPLINISLVYKIVFVATR	QAQQITTTLSKSL-----	244
QY	243	SKERAKVKTGLVNGVFLIC	WCPFFICTWMDPFLHYIIP	PTINDVLIWFGVINSTFPMV	302
Db	245	KHERKAATKLGIVGVILL	CWLPTFTIDTMDVSLHFF	ITPPLVDFDIFWFAFNSACN	PII 304

A;Molecule type: mRNA
A;Residues: 95-259 <ULI>
A;Cross-references: EMBL:Z48153; NID:g984171; PID:CAA88170.1; PID:g984172
A;Experimental source: tissue brain
C;Superfamily: vertebrate rhodopsin
C;Keywords: neurotransmitter receptor

Query Match 29.4%; Score 529; DB 2; Length 406;
Best Local Similarity 35.4%; Pred. No. 9.9e-37;
Matches 111; Conservative 61; Mismatches 114; Indels 28; Gaps 6;

199 YIPGSIMLCVYVRIYLTAKEQARLISDANQKLQIGLEMKNCISQSK----- 244

b	202	YIPFLMLWLAYRIYIVTAK	-----QQIQM-LQKAGAISSKPKUAYLQHSIHRMKI	253
y	245	ERKAVKTLIGVMGVFLICW	CPFFICTVMDPLHYIIPPTLNDVLIFGFLYLNSTNPMVYA	304
b	254	ETKAAKTLICVINGCFCF	CMAPPFFVNIYDPFDIDYTPVKVMTAFMLGWIINSGLNPFPLYA	313
y	305	FFYPWFRKALKMML	318	

RESULT 4

36849 opamine receptor-like protein D14 - Japanese pufferfish
;Species: Fugu rubripes (Japanese pufferfish)
;Date: 27-Oct-1995 #sequence revision 27-Oct-1995 #text change 20-Jun-2000

;Accession: A56849
;Macrae, A.D.; Brenner, S.
enomics 25, 436-446, 1995
;Title: Analysis of the dopamine receptor family in the compact genome of the

;Accession: A56849
 ;Reference number: A56849; MUID:9530911; PMID:1189977
 ;Status: preliminary; not compared with conceptual translation
 ;Molecule type: DNA

;Residues: 1-459 <MAC>
;Cross-references: GB:X80174; NID:g1204089; PIDN:CAA56455.1; PID:g1204090
;Superfamily: vertebrate rhodopsin
;Keywords: neurotransmitter receptor

Query Match	28.3%;	Score 510.5;	DB 2;	Length 459;
Best Local Similarity	37.0%;	Pred. No. 3.9e-35;		
Matches 118:	Conservative	54:	Mismatches 110:	Indels 37: Gaps 8

31 LIILTTLVGNLIVIVSISHEFKQLHTP-TNWLIIHSMTATVDLLGCLVMPYSMVRSAEHCWY 89
| : | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
32 LITETTTIGNTTVCVAVMKFRHPISKVTNEFVI SLATSLLAVAILVNWPWKAAETEIMGFWP 91

90 FGEVFCIKHTSTDMILSSASIFHSFISIDRYAYAVCDPLRYAKAQNILVICWFIWSV 149
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
92 EGE - ECNTGVAENIMCTASTANICVISVDRYWATSSPFERYEKMTPKVACIMISVAWTL 150

[illegible]

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201 PGSIMLCVVYRIYLIKEQARLI-----SDANQKLIQIGUEMKNGISQSKER 246
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
207 DYATIMIVYTDYDTACKQITDPSAI EPAAESAOBPHSSMGNSI SMSECSFKNISFKET 266

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QY 247 KAVKTLGIVMGVFLICWCPFFICTVMDPFLHY-----LIPTLNDVLWFGYLNSTFN 299
Db 267 KVLKTLVINGVFCVCCWLPFFILNCMVPCPADDTTDFPCISSTTTFDVFVFWGWNSSLN 326
QY 300 PMVYAFYFVFWFRKALKOML 318
Db 327 PIYAFNAD-FRKAFFSILL 344

RESULT 5
151661
dopamine D1c receptor - African clawed frog (fragment)
C:Species: Xenopus laevis (African clawed frog)
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 13-Aug-1999
C:Accession: I51661
R:Sugamori, K.S.; Demchishyn, L.L.; Chung, M.H.; Miznik, H.B.
Proc. Natl. Acad. Sci. U.S.A. 91, 10536-10540, 1994
A:Title: D1A, D1B, and D1C dopamine receptors from Xenopus laevis.
A:Reference number: I51659; MUID:95024150; PMID:7937989
A:Accession: I51661
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-465 <SUG>
A:Cross-references: EMBL:U07865; NID:g559763; PIDN:AAA50830.1; PID:g559764
C:Superfamily: vertebrate rhodopsin
C:Keywords: neurotransmitter receptor

Query Match 27.6%; Score 497.5; DB 2; Length 465;
Best Local Similarity 34.5%; Pred. No. 4.8e-34;
Matches 118; Conservative 61; Mismatches 130; Indels 33; Gaps 8;

QY 6 NIINISCVKNWNSD-----VPASLYSLMWLIILTLVGNLIVIVSISHFQKLTHTP 56
Db 5 SIPNVTV--NVWHDLDVGNDSLRLTGLLLSLTLSTLGNLTIVCLAVTKFRLRSK 62
QY 57 -TNWLHSMATVDFLLGCLVMPYSVMSAEHCWYFGEVCKIHTSDIMLSSASIFHLGSF 115
Db 63 VTNFFVISLAVSDLFVALLVMPKATEVAGFWFGD-FCDTWAFDINCMSTASILNLCI 121
QY 116 ISIDRYAVCDPLRYKAKKNILVICVMIFISVPAVAFPMIFLELNFKGABEIIYKHV 175
Db 122 ISLDRYALASPFRYERKMTQVAFIMIGVAMTSLISFIPQLSWHKSHEADBELNGV 181
QY 176 HCRGGSVFFSKISGLVLTWMTSYIPGSMVLCVYRIYLIKQEARLISDAN-----OK 229
Db 182 NHTENCSSLNRTYAISSLSIFYPVIMIGTYRIYIAQTQIRRISSLERAVEHAQR 241
QY 230 LOIGLEMKNGISQS--KERVAVKTLGIVMGVFLICWCPFFICTVMDPFLHYIIP----- 281
Db 242 CSSRLSNENSLKTSFRKETKVLKTLISLNGVVFVFCWLPFFVLNCMIPFCHMLPGQNEPE 301
QY 282 -----PTLNDVLWFGYLNSTFNPMVYAFYFVFWFRKALKOML 318
Db 302 PPCVSETTFNIWFVFGWANSNLNPIYAFNAD-FRKAFTTIL 342

RESULT 6
150475
dopamine D1 receptor - goldfish
C:Species: Carassius auratus (goldfish)
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 13-Aug-1999
C:Accession: I50475
R:Prall, D.E.; Manelli, A.M.; Witte, D.G.; Lin, C.W.; Steffey, M.E.; Mackenzie, R.O.
Mol. Pharmacol. 44, 1113-1118, 1993
A:Title: Cloning and characterization of a truncated dopamine D1 receptor from goldfish
A:Reference number: I50475; MUID:94088471; PMID:8264547
A:Accession: I50475
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-363 <FRA>
A:Cross-references: GB:L08602; NID:g212949; PIDN:AAA16322.1; PID:g212950
C:Superfamily: vertebrate rhodopsin

C:Keywords: neurotransmitter receptor

Query Match 27.4%; Score 493.5; DB 2; Length 363;
Best Local Similarity 36.3%; Pred. No. 8.2e-34;
Matches 118; Conservative 59; Mismatches 117; Indels 31; Gaps 8;

QY 21 VPASLYSLMWLIILTLVGNLIVIVSISHFQKLTHTP-TNWLHSMATVDFLLGCLVMPYS 79
Db 23 VRVLTGCFSLVILSTLGNLTIVCAAVTKFRHLRSKVTNFFVVISLAVSDLLVAVLWPMK 82

QY 80 MVSRAEHCWYFGEVCKIHTSDIMLSSASIFHLSPISIDRYAVCDPLRYKAKKNILVI 139
Db 83 ATEVAGFWPFG-AFCDIWAFFDINCMSTASILNLCVISVDYWAISSPRYEKMTPRVA 141

QY 140 CVMIFISVPAVAFPMIFLELNFKGABEIIYKHVHC-----RGCSVFFSKISGLVT 193
Db 142 FVMISGAWTSLVLSF--IPVQLKWHKAQPIGFLVNASRRDLPTDNCSSLNRTYAISS 199

QY 194 FMTSFYIPGSMVLCVYRIYLIKQEARLIS--DANQKLQI-----GLEMKNG 239
Db 200 SLISFYIPVAIMIVTYTQIYRAQKQIRISALERAESAQIRHDSMGSGSNMDESSPK 259

QY 240 ISQSKERKAVKTLGIVMGVFLICWCPFFICTVMDPFLHY-----IIPTLNDVLWFGY 293
Db 260 LSKRETKVLKTLVINGVFCVCCWLPFFILNCMVPCCKTSNGLPCISPTTFDVFVFWG 319

QY 294 LNSTNPMVYAFYFVFWFRKALKOML 318
Db 320 ANSSLNPIIYAFNAD-FRRAFAILL 343

RESULT 7

QJ01278
histamine H2 receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 05-Nov-1999
C:Accession: QJ01278
R:Ruot, M.; Traiffort, E.; Arrang, J.M.; Leurs, R.; Schwartz, J.C.
Biochem. Biophys. Res. Commun. 179, 1470-1478, 1991
A:Title: Cloning and tissue expression of a rat histamine H2-receptor gene.
A:Reference number: QJ01278; MUID:92028890; PMID:1930188
A:Accession: QJ01278
A:Molecule type: DNA
A:Residues: 1-358 <RUA>
A:Cross-references: GB:S57565; NID:g236183; PIDN:AAB19935.1; PID:g236184
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein

F:22-45/Domain: transmembrane #status predicted <TM1>
F:58-81/Domain: transmembrane #status predicted <TM2>
F:93-113/Domain: transmembrane #status predicted <TM3>
F:136-159/Domain: transmembrane #status predicted <TM4>
F:178-203/Domain: transmembrane #status predicted <TM5>
F:234-260/Domain: transmembrane #status predicted <TM6>
F:267-288/Domain: transmembrane #status predicted <TM7>
F:4/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:220,311,315/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 27.0%; Score 486; DB 2; Length 358;
Best Local Similarity 34.0%; Pred. No. 3.4e-33;
Matches 117; Conservative 56; Mismatches 123; Indels 48; Gaps 7;

QY 11 SCVKRWNSDVPASLYSLMWLIILTLVGNLIVIVSISHFQKLTHTP-TNWLHSMATVDFL 70
Db 9 SCCLDSMALKVTISV--VLTTLITITAGNVVCLAVSLNRLRLSLTNCFCVSLAATDIL 66

QY 71 LGCLVMPYSVMSRAEHCWYFGEVCKIHTSDIMLSSASIFHLSPISIDRYAVCDPLRY 130
Db 67 LGLLVLPFSAIYQLSFTWSPFGHVFCNIYTSLDVMLCTASILNLFMSIDRYCAVTDPLRY 126

QY 131 KAKMNLICVMIFISVPAVAFPMIFLELNFKGABEIIYKHVHCRG-----CSVFF 185
Db 127 PVLVTPVRVAISLVFIWISITLSLSFLSHLGWNSRG-----TRGNDTFCKKQV 177


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QY 251 TLGIWGVFLICWCPFFICTVMDPFLHY-----IIPPTLNDVLIWFGYLNSTENP 300
Db 283 TLISINGVFCWCLWPPFIILNCWVFFCDRSPGHQAGLPCVSETTFDIFWVFGWANSLLNP 342
QY 301 MYVAFYPMFRKALKMML 318
Db 343 IIAFNAD-FRKVFSSLL 359

RESULT 11
I51659
dopamine D1A receptor - African clawed frog (fragment)
C:Species: Xenopus laevis (African clawed frog)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 13-Aug-1999
C:Accession: I51659
R:Sugamori, K.S.; Demchyshyn, L.L.; Chung, M.H.; Niznik, H.B.
Proc. Natl. Acad. Sci. U.S.A. 91, 10536-10540, 1994
A:Title: D1A, D1B, and D1C dopamine receptors from Xenopus laevis.
A:Reference number: I51659; MUID:95024150; PMID:7937989
A:Accession: I51659
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-451 <SUG>
A:Cross-references: EMBL:U07863; NID:G559759; PIDN:AAA50828.1; PID:G559760
C:Superfamily: vertebrate rhodopsin
C:Keywords: neurotransmitter receptor

Query Match 26.7%; Score 480; DB 2; Length 451;
Best Local Similarity 34.5%; Pred. No. 1.4e-32;
Matches 111; Conservative 56; Mismatches 117; Indels 38; Gaps 7;

QY 31 LIILTLVGNLIVIVISISHFKOLHTP-TNWLHSMATVDLGLVMPYSMVSAEHCWY 89
Db 31 VILSTLGNLTUACAVIRFHLRSKVTNFFVLSLAVSDLLVAVLWMPKVAEIAAGFWP 90
QY 90 FGEVFCIKHTSDIMLSSASIFHLSFISIDRYAVCDPLRYKAKMNLIVCMIFISWSV 149
Db 91 FG-TCNIWAFDLMCSTASILNLCVISVDRYWAISPPFYEKMTPKVAFMIGVWTL 149
QY 150 PAVFAFGMFLFLEINFKGAEIYY-----KHVHRCGCVSFFSKISGLVTFMTSFYIP 203
Db 150 SVLISF-IPVQLNWHKAKTTFFDLNLTHTDNCDSLNRTVAISSLSISFYIPVA 207
QY 204 IMLCVYRILYLTAKQARLISDANKQLQIGLEMKGISQ-----SKER 246
Db 208 IMIVTYRIRAAQIRISALERAARVAHAKNCONSTNRNSLDCQOPSSLSKTSFKRET 267
QY 247 KAVKTLGIWGVFLICWCPFFICTVMDPFLH-----YIIPPTLNDVLIWFGYLS 296
Db 268 KVLKTLVIMGVFCWCLWPPFIILNCIVPCDPSLITSGTEPFCISSTTFDVFVFGWANS 327
QY 297 TPNMVMYAFYPMFRKALKMML 318
Db 328 SLNPIIYAFNAD-FRKAFSNLL 348

RESULT 12
S68423
serotonin receptor 1D alpha - rabbit
N:Alternate names: 5-hydroxytryptamine receptor 1D alpha (5-HT1Dalpha)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 05-Nov-1999
C:Accession: S68423
R:Harwood, G.; Lockyer, M.; Giles, H.; Fairweather, N.
FEBS Lett. 377, 73-76, 1995
A:Title: Cloning and characterisation of the rabbit 5-HT (1D-alpha) rec
A:Reference number: S68422; MUID:96130324; PMID:8543023
A:Accession: S68423
A>Status: preliminary; nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-377 <HAR>
A:Cross-references: EMBL:Z50162; NID:G1004281; PIDN:CAA90530.1; PID:G1004282
C:Superfamily: octopamine receptor type I
```

C:Keywords: neurotransmitter receptor

Query Match 26.4%; Score 475; DB 2; Length 377;
Best Local Similarity 32.0%; Pred. No. 3e-32;
Matches 112; Conservative 62; Mismatches 120; Indels 56; Gaps 7;

QY 21 VRASLYSLMVLILTLVGNLIVIVISISHFKOLHTP-TNWLHSMATVDLGLVMPYSM 80
Db 37 LKISLAVLSVITLAVLSNAPVLTLLTRKLTNPANYLIGSLATDLLVSLVMPISI 96

QY 81 VRSAEHCWYFGEVFCIKHTSDIMLSSASIFHLSFISIDRYAVCDPLRYKAKMNLIVIC 140
Db 97 AVTIHTWVFGVQLCDIWSDDITCTASILHLCVIALDRYWAITDALEYSKERTAGHAA 156

QY 141 VMFISWSVPVAFAGMIFLEINFKGAEIYYKHVHRCGCVSFFSKIS-GWLTFTWTSFY 199
Db 157 AMIAVVAISICISIPPLFWR-QAKAHEV-----SDCLVNTSQISYTIYSTCGAFY 207

QY 200 IFGSIMLCVYRYLYIAKEQ-----ARLISDA----- 226
Db 208 IPSVILLIYGRYMAARNRILNPPSLYGRKRTTAHLITGSAGSSLCSPSLGEGHSHS 267

QY 227 -----NOKLQIGLEMKNGISQSKERKAVKTLGIWGVFLICWCPFFICTVMDPFL 276
Db 268 AGSPLEFNPVRIKLADSVLERKRIISAARERKATKTLGIILGAFICGWLPPFFVASLVLPIC 327

QY 277 H--YIIPPTLNDVLIWFGYLSNTPMVMYAFYPMFRKALKMML-FGKIP 323
Db 328 RDSWMPGLEDFFTWLGYNLSLNPITYTVFNEDFRQAFORVIHFRKAF 377

RESULT 13

AS3279

serotonin receptor 1D - human

N:Alternate names: 5-hydroxytryptamine receptor 1D (5-HT1D); 5HT-1D alpha receptor
C:Species: Homo sapiens (man)

C:Date: 12-May-1994 #sequence_revision 12-May-1994 #text_change 05-Nov-1999

C:Accession: A53279; A44136

R:Hamblin, M.W.; Metcalf, M.A.

Mol. Pharmacol. 40, 143-148, 1991

A:Title: Primary structure and functional characterization of a human 5-HT-1D-type serot

A:Reference number: A53279; MUID:91342595; PMID:1652050

A:Accession: A53279

A:Molecule type: DNA

A:Residues: 1-377 <HAM>

A:Cross-references: GB:M89955; NID:G177771; PIDN:AAA35491.1; PID:G177772

R:Weinshank, R.L.; Zgombick, J.M.; Macchi, M.J.; Branchek, T.A.; Hartig, P.R.

Proc. Natl. Acad. Sci. U.S.A. 89, 3630-3634, 1992

A:Title: Human serotonin 1D receptor is encoded by a subfamily of two distinct genes: 5-

A:Reference number: A44136; MUID:92228840; PMID:1565658

A:Accession: A44136

A:Molecule type: mRNA

A:Residues: 1-377 <WEI>

A:Cross-references: GB:M81589; NID:G338023; PIDN:AAA60315.1; PID:G338024

C:Genetics:

A:Gene: GDB:HTR1D

A:Cross-references: GDB:I32416; OMIM:182133

A:Map position: lp36.3-lp34.3

A:Introns: #status absent

C:Superfamily: octopamine receptor type I

C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transme

Query Match 26.3%; Score 474; DB 2; Length 377;
Best Local Similarity 33.3%; Pred. No. 3.6e-32;
Matches 120; Conservative 57; Mismatches 111; Indels 72; Gaps 11;

QY 21 VRASLYSLMVLILTLVGNLIVIVISISHFKOLHTP-TNWLHSMATVDLGLVMPYSM 80
Db 37 LKISLAVLSVITLAVLSNAPVLTLLTRKLTNPANYLIGSLATDLLVSLVMPISI 96

QY 81 VRSAEHCWYFGEVFCIKHTSDIMLSSASIFHLSFISIDRYAVCDPLRYKAKMNLIVIC 140
Db 97 AVTIHTWVFGVQLCDIWSDDITCTASILHLCVIALDRYWAITDALEYSKERTAGHAA 156

QY 141 VMIFISWSVPVAFQMIFFLELNFPGABEIIYKHVCHRCGCSVPFSPKIS-GVLTFTWTSFY 199
Db 157 TMAIWAISICISIPPLFWR-QAKAQEEM-----SDCLVNTSQISYTIYSTCGAFY 207
QY 200 IFGSIMLCVYRIYIAKEQ-----ARLISDA-----NQLQIG----- 233
Db 208 IPSVLLIILYGRYIARNRILNPPSLYGRKRTTAHLITGSAGSSILCSLNSLHGHSHS 267
QY 234 -----LEMKNGISQSKERKAVKTLGLVMGVFLICWCPEFFICTVMDP- 274
Db 268 AGSPLEFNHVKIKLADSALERK-ISAARERKATKILGILGAFIICWLPFFVWSLVLP 326
QY 275 -----FLHVIIPPTLNDVLIWFGYLNSTFNPVYAFFWFRKALKMMLFGKI--FOKDS 327
Db 327 CRDSCWIIH-----PALFDFFTWILGYLNSLINPIYTVFNEEPROA-----FOKIVPRKAS 377

RESULT 14
I77467
serotonin receptor 1D - rat
N:Alternate names: 5-hydroxytryptamine receptor 1D (5-HT1D)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 24-Nov-1999
C:Accession: I77467
R:Hamblin, M.W.; McGuffin, R.W.; Metcalf, M.A.; Dorsa, D.M.; Merchant, K.M.
Mol. Cell. Neurosci. 3, 578-587, 1992
A:Title: Distinct 5-HT1B and 5-HT1D serotonin receptors in rat: structural and pharmacol
A:Reference number: 157683
A:Accession: I77467
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-374 <RES>
A:Cross-references: GB:M89953; NID:Q202544; PIDN:AAA40614.1; PID:Q202545
C:Superfamily: octopamine receptor type I
C:Keywords: neurotransmitter receptor

Query Match 26.3%; Score 473; DB 2; Length 374;
Best Local Similarity 32.1%; Pred. No. 4.4e-32;
Matches 117; Conservative 62; Mismatches 116; Indels 70; Gaps 10;
QY 17 WGNVDV-----RASLYSLMVLIIITLVGNLIVIVSISHPKQLHTPTNLIHSMATVDFLLG 72
Db 26 WDEVLQALRISLVVLSITLTLVLSNAFVLTILLTKLHTPANYLIGSLATTOLIVS 85
QY 73 CLVMPYSWVRSAEHCWYFGEVFCIKHTSTDMLSASIFHLSPISIDRYAVCDPLRYKA 132
Db 86 ILVMPISIAVTTTTRTNFQQLCDIWSVSDITCCTASILHLCVIALDRYWAITDALEYSK 145
QY 133 KMNILVICMIFISVPAVFAFGMIFLELNFPGABEIIYKHVCHRCGCSVPFSPKIS-GV 191
Db 146 RTAGHAAMIAAVWAISICISIPPLFWR-QATAHEM-----SDCLVNTSQISYTI 196
QY 192 LTFMTSFYIPGIMLCVYRIYIAKEQ-----ARLISDA----- 226
Db 197 YSTCGAFYIPSLIILYGRYIARNRILNPPSLYGRKRTTAHLITGSAGSSILCSLNS 256
QY 227 -----NQ-----KIQIGLEMKNGISQSKERKAVKTLGLVMGVFLICWCPEFFI 268
Db 257 LHESHHTVGSPLFFNQVQIKLADSILERKRISAARERKATKILGILGAFIICWLPFFV 316
QY 269 CTVMDP-----FLHVIIPPTLNDVLIWFGYLNSTFNPVYAFFWFRKALKMMLFGKI 322
Db 317 VSLVLPICRDCWIIH-----PALFDFFTWILGYLNSLINPIYTVFNEEPROAQRV 369
QY 323 FOKDS 327
Db 370 FRKAS 374

RESULT 15
JH0449
histamine H2 receptor - human

C:Species: Homo sapiens (man)
C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 24-Nov-1999
C:Accession: JH0449; I52319
R:Gantz, I.; Munzert, G.; Tashiro, T.; Schaeffer, M.; Wang, L.; Delvalle, J.; Yamada, T.
Biochem. Biophys. Res. Commun. 178, 1386-1392, 1991
A:Title: Molecular cloning of the human histamine H2 receptor.
A:Reference number: JH0449; MUID:91337087; PMID:1714721
A:Accession: JH0449
A:Molecule type: DNA
A:Residues: 1-359 <GAN>
A:Cross-references: GB:M64799; NID:G184087; PIDN:AAA58647.1; PID:G184088
R:Nishi, T.; Koike, T.; Oka, T.; Maeda, M.; Futai, M.
Biochem. Biophys. Res. Commun. 210, 616-623, 1995
A:Title: Identification of the promoter region of the human histamine H2-receptor gene.
A:Reference number: I52319; MUID:95275318; PMID:7755641
A:Accession: I52319
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-359 <RES>
A:Cross-references: GB:D49783; NID:G728495; PIDN:BAAO8618.1; PID:G728496
C:Comment: Histamine is important in the regulation of gastric acid secretion.
C:Genetics:
A:Gene: GDB:HRH2
A:Cross-references: GDB:391259; OMIM:142703
A:Map position: 5pter-Sqter
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein
F:23-44/Domain: transmembrane #status predicted <TM1>
F:58-81/Domain: transmembrane #status predicted <TM2>
F:93-114/Domain: transmembrane #status predicted <TM3>
F:135-159/Domain: transmembrane #status predicted <TM4>
F:181-204/Domain: transmembrane #status predicted <TM5>
F:235-258/Domain: transmembrane #status predicted <TM6>
F:268-289/Domain: transmembrane #status predicted <TM7>

Query Match 26.2%; Score 472.5; DB 2; Length 359;
Best Local Similarity 32.6%; Pred. No. 4.6e-32;
Matches 106; Conservative 64; Mismatches 124; Indels 31; Gaps 5;
QY 18 SNDVRASLYSLMVLIIITLVGNLIVIVSISHPKQLHTPTNLIHSMATVDFLLGCLVMP 77
Db 14 STACKITITVTLAVLILITVAGNVVYVCLAVGLNRRRLNLTNCFIVSLAITDILLGLVLP 73
QY 78 YSMVRSAEHCWYFGEVFCIKHTSTDMLSASIFHLSPISIDRYAVCDPLRYKAKMNTL 137
Db 74 FSAITQLSCKWSFGVFCNITYTSLDMLCTABILNLFMISLDRYCAVMDPLRYPVLTVP 133
QY 138 VICVMIFISWSVPVAFQMIFFLELNFPGABEIIYKHVCHRCGCSVPFSPKISGVLTFMTS 197
Db 134 RVAISLVLIVISITLSFLSIHLGWSNRNETS---KGNHTTSKCKVQVNVYGLVDGLVT 190
QY 198 FYIPGIMLCVYRIYIAKEQARLISDANQKIQIGLEMKNGISQSK-----ERKAVKTL 252
Db 191 FYLPLIMCITYIRIFKVARDOAKRI-----NHISWKAATIREHKATVTL 236
QY 253 GLVMGVFLICWCPEFFICTVM-----DPLHVIIPPTLNDVLIWFGYLNSTFNPVYAFFY 307
Db 237 AAVMGAFICWPFYTAFFYRGLRGDDAINEV-----LEAIVLWLGANSALNPILYAALN 292
QY 308 PWFRKALKMMLFGKIFOKDSRCKL 332
Db 293 RDRFTGYQQLFCRLANRNRSKTS 317

Search completed: October 8, 2004, 10:21:18
Job time : 21 secs